

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 10:02:18 ; Search time 58.3333 Seconds
(without alignments)
54.421 Million cell updates/sec

Title: US-09-549-186b-7

Perfect score: 104

Sequence: 1 CGSGVRGDFGSLAPRVARQL 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 95 | 91.3 | 19 | ABU08642 | Foot and mouth dis |
| 2 | 95 | 91.3 | 20 | AAV94587 | Envelope gene epit |
| 3 | 95 | 91.3 | 31 | AAV30107 | Sequence of VP1 ca |
| 4 | 95 | 91.3 | 31 | AAV30728 | Foot-and-mouth dis |
| 5 | 95 | 91.3 | 31 | AAW17082 | Foot and mouth dis |
| 6 | 95 | 91.3 | 35 | AAV68501 | Target antigenic p |
| 7 | 95 | 91.3 | 75 | AAV68528 | Synthetic foot and |
| 8 | 95 | 91.3 | 216 | AAV30205 | Sequence encoded b |
| 9 | 95 | 91.3 | 220 | AAV30195 | Sequence encoded b |

| | | | | | | |
|----|----|------|-----|----|----------|--------------------|
| 10 | 95 | 91.3 | 233 | 4 | AAV30204 | Sequence encoded b |
| 11 | 95 | 91.3 | 405 | 4 | AAV30202 | Sequence encoded b |
| 12 | 95 | 91.3 | 406 | 4 | AAV30203 | Sequence encoded b |
| 13 | 95 | 91.3 | 609 | 4 | AAV30206 | Sequence encoded b |
| 14 | 92 | 88.5 | 31 | 18 | AAW17086 | Foot and mouth dis |
| 15 | 91 | 87.5 | 31 | 18 | AAW17087 | Foot and mouth dis |
| 16 | 89 | 85.6 | 31 | 18 | AAW17084 | Foot and mouth dis |
| 17 | 88 | 84.6 | 31 | 18 | AAW17083 | Foot and mouth dis |
| 18 | 88 | 84.6 | 31 | 18 | AAV68502 | Target antigenic p |
| 19 | 87 | 83.7 | 35 | 21 | AAV68508 | Target antigenic p |
| 20 | 87 | 83.7 | 46 | 21 | AAV68503 | Target antigenic p |
| 21 | 87 | 83.7 | 65 | 21 | AAV68527 | Synthetic foot and |
| 22 | 87 | 83.7 | 75 | 21 | AAV68529 | Synthetic foot and |
| 23 | 85 | 81.7 | 19 | 24 | ABU08643 | Foot and mouth dis |
| 24 | 85 | 81.7 | 35 | 7 | AAV60895 | Peptide containing |
| 25 | 85 | 81.7 | 35 | 9 | AAV82746 | VP1(A12,119) contg |
| 26 | 80 | 76.9 | 18 | 4 | AAV30110 | Sequence of VP1 ca |
| 27 | 77 | 74.0 | 20 | 14 | AAV38543 | Foot and Mouth Dis |
| 28 | 77 | 74.0 | 20 | 14 | AAW1793 | Foot and Mouth Dis |
| 29 | 76 | 73.1 | 20 | 18 | AAW17085 | Foot and Mouth Dis |
| 30 | 71 | 68.3 | 35 | 21 | AAV68508 | Consensus antigen |
| 31 | 71 | 68.3 | 31 | 18 | AAV30198 | Sequence encoded b |
| 32 | 71 | 68.3 | 233 | 4 | AAV30209 | Sequence of antige |
| 33 | 67 | 64.4 | 20 | 5 | AAV40103 | Sequence at antige |
| 34 | 67 | 64.4 | 216 | 5 | AAV40085 | Sequence of foot a |
| 35 | 64 | 61.5 | 248 | 4 | AAV30207 | Consensus antigen |
| 36 | 63 | 60.6 | 35 | 21 | AAV68509 | Consensus antigen |
| 37 | 63 | 60.6 | 55 | 21 | AAV68533 | Synthetic foot and |
| 38 | 58 | 55.8 | 218 | 4 | AAV30196 | Sequence encoded b |
| 39 | 56 | 53.8 | 28 | 4 | AAV30316 | Sequence of VP1 ca |
| 40 | 56 | 53.8 | 213 | 21 | AAW15428 | Foot and mouth dis |
| 41 | 56 | 53.8 | 213 | 21 | AAW15397 | Foot and mouth dis |
| 42 | 56 | 53.8 | 213 | 21 | AAW15398 | Foot and mouth dis |
| 43 | 56 | 53.8 | 213 | 21 | AAW15402 | Foot and mouth dis |
| 44 | 54 | 51.9 | 36 | 7 | AAV60895 | Peptide containing |
| 45 | 54 | 51.9 | 36 | 9 | AAV82747 | VP1(A24,C) contg. |

ALIGNMENTS

| | | |
|----------|----------|--|
| RESULT 1 | ABU08642 | ABU08642 standard; peptide: 19 AA. |
| XX | AC | ABU08642; |
| XX | DE | 04-JUN-2003 (first entry) |
| XX | XX | Foot and mouth disease virus (FMDV) VP1-A12141-159, variant FP. |
| XX | XX | Foot and mouth disease virus; FMDV; VP1-A12 region; immunosuppressive; |
| XX | KW | antiflammatory; antiarthritic; antirheumatic; dermatological; |
| XX | KW | antidiabetic; antinaemic; neuroprotective; vaccine; |
| XX | KW | anti-metallochionein antibody; humoral immune response; |
| XX | KW | autoimmune disease; Grave's disease; rheumatoid arthritis; |
| XX | KW | systemic lupus erythematosus; Type 1 diabetes; pernicious anaemia; |
| XX | KW | multiple sclerosis; Sjorgen's disease. |
| XX | OS | Foot and mouth disease virus. |
| XX | PN | US2003007973-A1. |
| XX | PD | 09-JAN-2003. |
| XX | PF | 24-JUN-2002; 2002US-0178909. |
| XX | PR | 22-JUN-2001; 2001US-300346P. |
| XX | PA | (LYNE/) LYNES M A. |
| XX | PI | Lynes MA; |
| XX | XX | |

DR WPI; 2003-353082/33.
 XX
 PT Treating autoimmune diseases, e.g. Grave's disease, arthritis, lupus,
 PT or diabetes by administering a composition consisting of an
 PT anti-metallothionein antibody to stimulate a humoral immune response in
 PT a subject -
 XX
 PS Example 7; Fig 9; 24pp; English.
 XX
 CC The invention describes a method of treating a subject comprising
 CC administering to the subject a composition consisting of an
 CC anti-metallothionein antibody to stimulate a humoral immune response in
 CC a subject. The methods and compositions are useful for treating
 CC autoimmune diseases, e.g. Grave's disease, rheumatoid arthritis,
 CC systemic lupus erythematosus, Type 1 diabetes, pernicious anaemia,
 CC multiple sclerosis or Sjogren's disease. This is the amino acid
 CC sequence of foot and mouth disease virus (FMDV) VPI-A12141-159 region
 CC used as an immunogen.
 XX
 SQ Sequence 19 AA;
 Query Match 91.3%; Score 95; DB 24; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GSGVRGDFGSLAPRVARQL 20
 DB 1 GSGVRGDFGSLAPRVARQL 19
 RESULT 2
 ID AAY94587 standard; Peptide: 20 AA.
 AC AAY94587;
 XX
 DT 10-JAN-2001 (first entry)
 XX
 DE Envelope gene epitope of foot and mouth disease virus.
 DE Hepatitis B virus nucleocapsid antigen; HBcAg; T cell epitope;
 KW cytolytic T lymphocyte; immunogenic; ICE; CTL; FMDV;
 KW immunodominant core epitope; immunisation; envelope gene.
 XX
 OS Foot and mouth disease virus.
 XX
 PN WO200026385-A1.
 XX
 PD 11-MAY-2000.
 XX
 PF 05-NOV-1999; 99WO-0526291.
 XX
 PR 05-NOV-1998; 98US-0107169.
 XX
 PA (POMD-) POWDERJECT VACCINES INC.
 XX
 PI Fuller DL, Fuller JT;
 XX
 DR WPI; 2000-451623/39.
 XX
 PT Use of expression vector for nucleic acid immunization that comprises
 PT promoter and recombinant nucleic acid sequences encoding Hepatitis B
 PT core antigen and T cell epitope from antigen -
 XX
 PS Example 6; Page 39; 55pp; English.
 XX
 CC The present invention relates to an immunogenic recombinant
 CC nucleic acid molecule. The molecule consists of a modified hepatitis
 CC B virus nucleocapsid antigen (HBcAg) with a T cell epitope sequence
 CC inserted within the HBcAg. The creation of a unique restriction site
 CC in HBcAg facilitated the insertion of the T cell epitope into the DNA
 CC encoding the immunodominant core epitope of the HBcAg. An example of a
 CC suitable insertion epitope is the present sequence, the

CC neutralisation epitope from the foot and mouth disease virus envelope
 CC gene. Alternatively other T cell epitopes may be inserted
 CC (AAY94583, AAY94584, AAY94585, AAY94586, AAY94588). The recombinant
 CC nucleic acid molecule may then be used as a reagent in various nucleic
 CC acid immunisation strategies. The advantage of this method of
 CC immunisation is that the nucleic acid reagents that encode hybrid HBcAg
 CC generate an extremely high frequency cellular immune response against
 CC the CTL epitope.
 XX
 SQ Sequence 20 AA;
 Query Match 91.3%; Score 95; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GSGVRGDFGSLAPRVARQL 20
 DB 1 GSGVRGDFGSLAPRVARQL 19
 RESULT 3
 ID AAP30107 standard; Peptide: 31 AA.
 AC AAP30107;
 XX
 DT 03-APR-1992 (first entry)
 XX
 DE Sequence of VPI capsid protein residues 130-160 from the amino-
 DE terminus, FMDV, Tubingen type A, subtype 12, strain 119.
 XX
 KW Antigen; Picornavirus; capsid protein; antibody; detection;
 KW vaccine; diagnosis.
 XX
 OS Foot and mouth disease virus.
 XX
 PN WO8303547-A.
 XX
 PD 27-OCT-1983.
 XX
 PF 14-APR-1983; 83WO-0002644.
 XX
 PR 25-MAR-1983; 83US-0478847.
 PR 14-APR-1982; 82US-0368308.
 PR 20-SEP-1984; 84US-0653475.
 PR 18-DEC-1984; 84US-0682819.
 XX
 PA (BITT/) BITTLE J L.
 PA (SCR-) SCRIPPS CLINIC & RE.
 XX
 PI Bittle JL, Lerner RA;
 XX
 DR WPI; 1983-807942/44.
 XX
 PT Antigenic peptide(s) corresp. to picornavirus capsid protein -
 PT useful in prodn. of vaccines and in diagnostic tests
 XX
 PS Example; Page 26; 90pp; English.
 XX
 CC The peptides of the invention corresp. to a region on the antigenic
 CC picornavirus capsid protein. The capsid protein FMDV VPI or polio
 CC virus VPI. When linked to carriers the peptides are immunogenic.
 CC Dose is 20 ug-2mg peptide for inoculations.
 XX
 SQ Sequence 31 AA;
 Query Match 91.3%; Score 95; DB 4; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GSGVRGDFGSLAPRVARQL 20
 DB 11 GSGVRGDFGSLAPRVARQL 29

RESULT 4
AAP50728 standard; protein; 31 AA.
ID AAP50728
XX
AC AAP50728;
XX
DT 23-OCT-1991 (first entry)
XX
DE Foot-and-mouth disease antigenic peptide.
XX
KW Foot-and-mouth disease; vaccine; antigen;
XX
OS Foot-and-mouth disease virus.
XX
PN US4544500-A.
XX
PD 01-OCT-1985.
XX
PF 18-DEC-1984; 84US-0682819.
XX
PR 18-DEC-1984; 84US-0682819.
XX
PA (SCRI-) SCRIPPS CLINIC & RESEARCH FOUNDATION.
XX
PI Bittle JL, Lerner RA;
XX
DR WPI: 1985-262823/42.
XX
PT Synthetic foot and mouth disease antigen - comprising 20 amino acid
XX
PS peptide corresp. to virus protein VP1.
XX
SQ Disclosure; page 4; 7pp; English.
XX
CC The peptide corresponds to amino acids 130-160 of the foot and mouth
XX
CC disease virus VP1 protein. It represents a monospecific synthetic
XX
CC antigenic determinant. The peptide can be used to vaccinate animals,
XX
CC esp. swine and cattle, against the virus with a single inoculation.
XX
SQ Sequence 31 AA;
XX
Query Match 91.3%; Score 95; DB 6; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 2 GSGVGRDGFSLAPRYARQL 20
DB 11 GSGVGRDGFSLAPRYARQL 29
XX
RESULT 5
AAW17082
ID AAW17082 standard; peptide; 31 AA.
XX
AC AAW17082;
XX
DT 13-JUN-1997 (first entry)
XX
DE Foot and mouth disease virus G-H loop of protein VP-1.
XX
KW Foot and mouth disease; aphthovirus; vaccine; antigen; epitope;
XX
KW immunogen; G-H loop; VP-1; deletion; mutant; binding site removal;
XX
KW antibody; non-infectious; attenuated.
XX
OS Foot and mouth disease virus.
XX
PN US5612040-A.
XX
PD 18-MAR-1997.
XX
PF 07-APR-1995; 95US-0418716.
XX

PR 07-APR-1995; 95US-0418716.
XX
XX (USDA) US SEC OF AGRIC.
XX
PI Baxt B, Bernstein A, Kang AS, Mason PW, Reider E;
XX
DR WPI: 1997-192081/17.
XX
PT Genetically modified foot-and-mouth disease virus - lacks
XX
PS cell-binding site and is non-infectious, useful in vaccines
XX
SQ Disclosure; Figure 1; 10pp; English.
XX
CC AAW17082 represents amino acids 130-163 of wild-type foot and mouth
XX
CC disease (FMD) virus VP-1 structural protein. The sequence represents
XX
CC the G-H loop, a flexible loop between the G and H beta strands of VP-1.
XX
CC The G-H loop is the main antigenic site of VP-1 and is also involved in
XX
CC cell binding. The FMD virus G-H loop peptide can be modified in a FMD
XX
CC virus by deletion of the amino acid (aa) sequence
XX
CC Gly-Val-Arg-Gly-Asp-Phe (aa 142-147) and replacing this sequence with the
XX
CC sequence Asn-Pro. This results in the virus retaining its immunogenicity
XX
CC but is not infectious because the cell binding site has been removed. The
XX
CC genetically modified FMD virus is useful in vaccines against the
XX
XX disease.
XX
SQ Sequence 31 AA;
XX
Query Match 91.3%; Score 95; DB 18; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 2 GSGVGRDGFSLAPRYARQL 20
DB 11 GSGVGRDGFSLAPRYARQL 29
XX
RESULT 6
AAV68501
ID AAV68501 standard; peptide; 35 AA.
XX
AC AAV68501;
XX
DT 05-MAY-2000 (first entry)
XX
DE Target antigenic peptide derived from amino acids 134-169 of VP1.
XX
KW Antigenic peptide: VP1 capsid protein; FMDV strain A12; epitope;
XX
KW helper T-cell epitope; immune response; vaccine; FMDV infection.
XX
OS Foot and mouth disease virus.
XX
PN WO966954-A1.
XX
PD 29-DEC-1999.
XX
PF 21-JUN-1999; 99WO-US13921.
XX
PR 20-JUN-1998; 98US-0100600.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
XX Wang CY, Shen M;
XX
PI WPI: 2000-160563/14.
XX
DR Synthetic peptide used in protecting animals against Foot-and-Mouth
XX
PT Disease Virus infections comprises a helper T-cell epitope and a
XX
PS Foot-and-Mouth Disease Virus epitope conjugate -
XX
PS Claim 1; Page 45; 115pp; English.
XX
CC The present sequence represents a target antigenic peptide derived from
XX
CC the VP1 capsid protein of Foot and Mouth Disease Virus (FMDV) strain A12.

CC The peptide is used to design synthetic epitopes, which are conjugated
 CC to a helper T-cell epitope and optionally an immunostimulator sequence.
 CC The peptides are covalently linked to each other, preferably by peptide
 CC bonds generated through direct synthesis. The synthetic vaccines of the
 CC invention require lower levels of biosecurity, have a reduced loss of
 CC immunogenic activity, are less prone to product instability due to
 CC lot-to-lot variability and do not need periodic revision due to
 CC antigenic variation in the field. The peptides are used as immunogens
 CC in vaccines to generate an enhanced immune response against a FMDV
 CC antigen in animals, such as swine, cattle, sheep, goats and susceptible
 CC wild species. They can also be used to diagnose FMDV infection in a
 CC mammal.

XX Sequence 35 AA:

QY Query Match 91.3%; Score 95; DB 21; Length 35;
 Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 GSGVRGDFGSLAPRVARQL 20
 7 GSGVRGDFGSLAPRVARQL 25

RESULT 7
 AAY68528
 ID AAY68528 standard; peptide; 75 AA.
 AC AAY68528;
 XX
 DT 05-MAY-2000 (first entry)
 XX
 DE Synthetic foot and mouth disease virus immunogen.
 XX
 KM Antigenic peptide; VP1 capsid protein; serotype Asia; epitope;
 KM helper T-cell epitope; immune response; vaccine; FMDV infection.
 XX
 OS Synthetic.
 OS Yersinia sp.
 OS Foot and mouth disease virus.

XX Key Location/Qualifiers
 FH Peptide 1..16
 FT /note= "Yersinia Invasin domain (immunostimulator
 FT peptide"
 FT Peptide 17..18
 FT /note= "spacer"
 FT Peptide 19..38
 FT /note= "autologous helper T-cell epitope derived
 FT from VP1 capsid protein"
 FT Peptide 39..40
 FT /note= "spacer"
 FT Peptide 41..75
 FT /note= "synthetic VP1 capsid protein epitope"

XX WO966954-A1.
 XX
 XX 29-DEC-1999.
 XX
 XX 21-JUN-1999; 99WO-0513921.
 XX
 XX 20-JUN-1998; 98US-0100600.
 XX
 XX (UNBI-) UNITED BIOMEDICAL INC.
 XX
 XX Wang CY, Shen M;
 XX
 XX WPI; 2000-160563/14.
 XX
 XX Synthetic peptide used in protecting animals against Foot-and-Mouth
 XX Disease Virus infections comprises a helper T-cell epitope and a
 XX Foot-and-Mouth Disease Virus epitope conjugate -

PS Claim 8; Page 96; 115pp; English.
 XX
 CC The present sequence represents a foot and mouth disease (FMDV) vaccine
 CC of the invention. The specification describes epitopes derived from an
 CC antigen of the VP1 capsid protein of FMDV. The VP1 epitopes are
 CC conjugated to a helper T-cell epitope and optionally an immunostimulator
 CC sequence. The peptides are covalently linked to each other, preferably
 CC by peptide bonds generated through direct synthesis. The synthetic
 CC vaccines of the invention require lower levels of biosecurity, have a
 CC reduced loss of immunogenic activity, are less prone to product
 CC instability and lot-to-lot variability and do not need periodic revision
 CC due to antigenic variation in the field. The peptides are used as
 CC immunogens in vaccines to generate an enhanced immune response against
 CC a FMDV antigen in animals, such as swine, cattle, sheep, goats and
 CC susceptible wild species. They can also be used to diagnose FMDV
 CC infection in a mammal.

XX Sequence 75 AA:

QY Query Match 91.3%; Score 95; DB 21; Length 75;
 Best Local Similarity 100.0%; Pred. No. 4.3e-07;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 GSGVRGDFGSLAPRVARQL 20
 47 GSGVRGDFGSLAPRVARQL 65

RESULT 8
 AAP30205
 ID AAP30205 standard; Protein; 216 AA.
 AC AAP30205;
 XX
 DT 29-JUL-1992 (first entry)
 XX
 DE Sequence encoded by direct expression vector pFM 10 which
 DE comprises the promoter and operator of the E. coli tryptophan
 DE operon Aas 1-211 of the VP3 gene linked to 4 Aas from pBR322.
 XX
 KM Vaccine; immunogen; antigen; viral protein.
 KM
 OS Foot and mouth disease virus.

XX EP68693-A.
 XX
 XX 05-JAN-1983.
 XX
 XX 11-JUN-1982; 82EP-0303040.
 XX
 XX 04-MAY-1982; 82US-0374855.
 XX
 XX 16-JUN-1981; 81US-0274103.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Kleid DG, Yansura DG;
 XX
 XX WPI; 1983-05055K/03.
 XX
 XX N-PADB; AAN30144.
 XX
 XX Polypeptide antigens of foot-and-mouth disease - obt'd. by
 XX recombinant DNA technology for vaccine prodn.
 XX
 XX Example; Page 36-37; 81pp; English.
 XX
 CC The inventors claim a polypeptide comprising at least one antigen of
 CC FMDV, or a fusion polypeptide of at least two antigens from at least
 CC two different FMDV strands, and encoding DNA. Pref. the fusion
 CC polypeptide has the sequence of two of the A, C, O, Asia-1, SAT 1,
 CC SAT 2 and SAT 3 type strains of the virus. The polypeptides pref.
 CC comprise Aas 55-177 or 1-210 of the VP3 virus. Fusion polypeptides
 CC may comprise Aas 1-210 fused to 8-210 of VP3 virus protein, pFM1,
 CC pFM2, pFM3, pFM10, pFM20, pFM81, pFM6, pFM4 and pFM5 are also

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CC claimed.
XX
SQ Sequence 216 AA;

Query Match
Best Local Similarity 91.3%; Score 95; DB 4; Length 216;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GSGVRGDFGSLAPRVARQL 20
   |||||
Db 141 GSGVRGDFGSLAPRVARQL 159

RESULT 9
AAP30195
ID AAP30195 standard; Protein; 220 AA.
XX
AC AAP30195;
XX
DT 29-JUL-1992 (first entry)
XX
DE Sequence encoded by VP3 gene of FMDV type A12 (7465).
XX
PA Vaccine; immunogen; antigen; viral protein.
XX
OS Foot and mouth disease virus.
XX
PN EP68693-A.
XX
PD 05-JAN-1983.
XX
PE 11-JUN-1982; 82EP-0303040.
XX
PR 04-MAY-1982; 82US-0374855.
XX
PR 16-JUN-1981; 81US-0274103.
XX
PA (GETH ) GENENTECH INC.
XX
PI K1eld DG, Yansura DG;
XX
DR WPI; 1983-05055K/03.
XX
DR N-PSDB; AAN30127.
XX
PT Polypeptide antigens of foot-and-mouth disease - obt'd. by
PT recombinant DNA technology for vaccine prodn.
XX
PS Disclosure; Fig 2; 81pp; English.
XX
CC The inventors claim a polypeptide comprising at least one antigen of
CC FMDV, or a fusion polypeptide of at least two antigens from at least
CC two different FMDV strands, and encoding DNA. Pref. the fusion
CC polypeptide has the sequence of two of the A, C, O, Asia-1, SAT 1,
CC SAT 2 and SAT 3 type strains of the virus. The polypeptides pref.
CC comprise AAs 55-177 or 1-210 of the VP3 virus. Fusion polypeptides
CC may comprise AAs 1-210 fused to 8-210 of VP3 virus protein. pFM1,
CC pFM2, pFM3, pFM10, pFM20, pFMB1, pFMC, pFMD, pFMR and pFMG are also
CC claimed.
XX
SQ Sequence 220 AA;

Query Match
Best Local Similarity 91.3%; Score 95; DB 4; Length 220;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GSGVRGDFGSLAPRVARQL 20
   |||||
Db 140 GSGVRGDFGSLAPRVARQL 158

RESULT 10
AAP30204
ID AAP30204 standard; Protein; 233 AA.
XX
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```
AC AAP30204;
XX
DT 29-JUL-1992 (first entry)
XX
DE Sequence encoded by pFM3 which comprises 17 AAs from the LE' gene
DE construction (fragment 3e), linked to a methionine AA (CNR cleavable),
DE linked to the AAs 1-211 of the VP3 FMDV A12, linked to 4 AAs from
DE pBR322.
XX
KM Vaccine; immunogen; antigen; viral protein.
XX
OS Foot and mouth disease virus and Escherichia coli.
XX
PN EP68693-A.
XX
PD 05-JAN-1983.
XX
PE 11-JUN-1982; 82EP-0303040.
XX
PR 04-MAY-1982; 82US-0374855.
XX
PR 16-JUN-1981; 81US-0274103.
XX
PA (GETH ) GENENTECH INC.
XX
PI K1eld DG, Yansura DG;
XX
DR WPI; 1983-05055K/03.
XX
DR N-PSDB; AAN30142.
XX
PT Polypeptide antigens of foot-and-mouth disease - obt'd. by
PT recombinant DNA technology for vaccine prodn.
XX
PS Example; Page 33-34; 81pp; English.
XX
CC The inventors claim a polypeptide comprising at least one antigen of
CC FMDV, or a fusion polypeptide of at least two antigens from at least
CC two different FMDV strands, and encoding DNA. Pref. the fusion
CC polypeptide has the sequence of two of the A, C, O, Asia-1, SAT 1,
CC SAT 2 and SAT 3 type strains of the virus. The polypeptides pref.
CC comprise AAs 55-177 or 1-210 of the VP3 virus. Fusion polypeptides
CC may comprise AAs 1-210 fused to 8-210 of VP3 virus protein. pFM1,
CC pFM2, pFM3, pFM10, pFM20, pFMB1, pFMC, pFMD, pFMR and pFMG are also
CC claimed.
XX
SQ Sequence 233 AA;

Query Match
Best Local Similarity 91.3%; Score 95; DB 4; Length 233;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GSGVRGDFGSLAPRVARQL 20
   |||||
Db 158 GSGVRGDFGSLAPRVARQL 176

RESULT 11
AAP30202
ID AAP30202 standard; Protein; 405 AA.
XX
AC AAP30202;
XX
DT 29-JUL-1992 (first entry)
XX
DE Sequence encoded by pFM1 which comprises 190 AAs from the LE' gene
DE construction linked to 6 AAs from the linker molecule (fragment 4),
DE linked to 205 AAs from the VP3 FMDV A12 (codons 7-211), linked to
DE 4 AAs from pBR322.
XX
KM Vaccine; immunogen; antigen; viral protein.
XX
OS Foot and mouth disease virus and Escherichia coli.
XX
PN EP68693-A.
```

```

XX 05-JAN-1983.
PD 11-JUN-1982; 82EP-0303040.
XX
XX 04-MAY-1982; 82US-0374855.
PR 16-JUN-1981; 81US-0274103.
XX
XX (GETH ) GENENTECH INC.
XX
XX Kleid DG, Yansura DG;
XX
XX WPI; 1983-05055K/03.
DR N-PSDB; AAN30140.
XX
XX Polypeptide antigens of foot-and-mouth disease - obtd. by
PT recombinant DNA technology for vaccine prodn.
XX
XX Example; Page 29-31; 81pp; English.
XX
XX The inventors claim a polypeptide comprising at least one antigen of
CC FMDV, or a fusion polypeptide of at least two antigens from at least
CC two different FMDV strands, and encoding DNA. Pref. the fusion
CC polypeptide has the sequence of two of the A, C, O, Asia-1, SAT 1,
CC SAT 2 and SAT 3 type strains of the virus. The polypeptides pref.
CC comprise AAs 55-177 or 1-210 of the VP3 virus. Fusion polypeptides
CC may comprise AAs 1-210 fused to 8-210 of VP3 virus protein. pFM1,
CC pFM2, pFM3, pFM10, pFM20, pFMB1, pFMC, pFMD, pFME and pFMC are also
CC claimed.
XX
XX Sequence 405 AA:
SQ
XX
XX Query Match 91.3%; Score 95; DB 4; Length 405;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-06;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 2 GSGVRGDFGSLAPRYARQL 20
DB 330 GSGVRGDFGSLAPRYARQL 348
XX
XX RESULT 12
XX AAP30203
XX ID AAP30203 standard; Protein; 406 AA.
XX
XX AAP30203;
XX
XX 29-JUL-1992 (first entry)
XX
XX Sequence encoded by pFM2 which comprises 190 AAs from the LE' gene,
DE linked to a methionine AA (CNR cleavable), linked to the AAs 1-211
DE of the VP3 FMDV A12 (codons 1-7 are derived from synthetic DNA, 8-211
DE are natural codons), linked to 4 amino acids from pBR322.
XX
XX Vaccine; Immunogen; antigen; viral protein.
XX
XX Foot and mouth disease virus and Escherichia coli.
XX
XX EP68693-A.
XX
XX 05-JAN-1983.
XX
XX 11-JUN-1982; 82EP-0303040.
XX
XX 04-MAY-1982; 82US-0374855.
PR 16-JUN-1981; 81US-0274103.
XX
XX (GETH ) GENENTECH INC.
XX
XX Kleid DG, Yansura DG;
XX
XX WPI; 1983-05055K/03.
DR N-PSDB; AAN30141.
XX

```

```

XX Polypeptide antigens of foot-and-mouth disease - obtd. by
PT recombinant DNA technology for vaccine prodn.
XX
XX Example; Page 31-32; 81pp; English.
XX
XX The inventors claim a polypeptide comprising at least one antigen of
CC FMDV, or a fusion polypeptide of at least two antigens from at least
CC two different FMDV strands, and encoding DNA. Pref. the fusion
CC polypeptide has the sequence of two of the A, C, O, Asia-1, SAT 1,
CC SAT 2 and SAT 3 type strains of the virus. The polypeptides pref.
CC comprise AAs 55-177 or 1-210 of the VP3 virus. Fusion polypeptides
CC may comprise AAs 1-210 fused to 8-210 of VP3 virus protein. pFM1,
CC pFM2, pFM3, pFM10, pFM20, pFMB1, pFMC, pFMD, pFME and pFMC are also
CC claimed.
XX
XX Sequence 406 AA:
SQ
XX
XX Query Match 91.3%; Score 95; DB 4; Length 406;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-06;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 2 GSGVRGDFGSLAPRYARQL 20
DB 331 GSGVRGDFGSLAPRYARQL 349
XX
XX RESULT 13
XX AAP30206
XX ID AAP30206 standard; Protein; 609 AA.
XX
XX AAP30206;
XX
XX 29-JUL-1992 (first entry)
XX
XX Sequence encoded by pFM 20 which is the polyanitgen comprising 190 AAs
DE coded by the LE' gene construction, linked to a methionine AA (CNR
DE cleavable), linked to the AAs 1-211 of the VP3 FMDV A12 (codons 1-7
DE are derived from synthetic DNA), linked to AAs 8-211 of the VP3
DE FMDV A12, linked to 4 AAs from pBR322.
XX
XX Vaccine; Immunogen; antigen; viral protein.
XX
XX Foot and mouth disease virus and Escherichia coli.
XX
XX EP68693-A.
XX
XX 05-JAN-1983.
XX
XX 11-JUN-1982; 82EP-0303040.
XX
XX 04-MAY-1982; 82US-0374855.
PR 16-JUN-1981; 81US-0274103.
XX
XX (GETH ) GENENTECH INC.
XX
XX Kleid DG, Yansura DG;
XX
XX WPI; 1983-05055K/03.
DR N-PSDB; AAN30145.
XX
XX Polypeptide antigens of foot-and-mouth disease - obtd. by
PT recombinant DNA technology for vaccine prodn.
XX
XX Example; Page 38-41; 81pp; English.
XX
XX The inventors claim a polypeptide comprising at least one antigen of
CC FMDV, or a fusion polypeptide of at least two antigens from at least
CC two different FMDV strands, and encoding DNA. Pref. the fusion
CC polypeptide has the sequence of two of the A, C, O, Asia-1, SAT 1,
CC SAT 2 and SAT 3 type strains of the virus. The polypeptides pref.
CC comprise AAs 55-177 or 1-210 of the VP3 virus. Fusion polypeptides
CC may comprise AAs 1-210 fused to 8-210 of VP3 virus protein. pFM1,

```

CC PFV2, PFV3, PFV10, PFV20, PFV61, PFV6C, PFVMD, PFVNF and PFVNG are also
CC claimed.
SQ Sequence 609 AA;
Query Match 91.3%; Score 95; DB 4; Length 609;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GSGVGRGDFGSLAPRVARQL 20
Db 331 GSGVGRGDFGSLAPRVARQL 349
|||||
RESULT 14
AAW17086
ID AAW17086 standard; peptide: 31 AA.
AC AAW17086;
XX
DF 13-JUN-1997 (first entry)
XX
DE Foot and mouth disease virus modified G-H loop of protein VP-1.
XX
KW Foot and mouth disease; aphthovirus; vaccine; antigen; epitope;
KW Immunogen; G-H loop; VP-1; deletion; mutant; binding site removal;
KW antibody; non-infectious; attenuated.
XX
OS Foot and mouth disease virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 15 /label= substitution
FT /note= "wild-type Arg replaced with Lys"
XX
PN US5612040-A.
XX
PD 18-MAR-1997.
XX
PE 07-APR-1995; 95US-0418716.
XX
PR 07-APR-1995; 95US-0418716.
XX
PA (USDA) US SEC OF AGRIC.
XX
PI Baxt B, Bernstein A, Kang AS, Mason PW, Reider E;
XX
DR WPI; 1997-192081/17.
XX
PT Genetically modified foot-and-mouth disease virus - lacks
PT cell-binding site and is non-infectious, useful in vaccines
XX
PS Disclosure; Figure 2; 10pp; English.
XX
CC AAW17083-W17088 are peptides representing mutant versions of amino acids
CC 130-163 of wild-type foot and mouth disease (FMD) virus VP-1 structural
CC protein. The mutants were made in order to investigate the requirements
CC of this region for cell binding. The sequences are mutant versions of
CC the G-H loop, a flexible loop between the G and H beta strands of VP-1)
CC VP-1, which is the main antigenic site of VP-1 and is also involved in
CC cell binding. The FMD virus G-H loop peptide can be modified in a FMD
CC virus by deletion of the amino acid (aa) sequence
CC Gly-Val-Arg-Gly-Asp-Phe (aa 142-147) and replacing this sequence with the
CC sequence Asn-Pro. This results in the virus retaining its immunogenicity
CC but is not infectious because the cell binding site has been removed. The
CC genetically modified FMD virus is useful in vaccines against the
CC disease.
XX
SQ Sequence 31 AA;
Query Match 88.5%; Score 92; DB 18; Length 31;
Best Local Similarity 94.7%; Pred. No. 5.2e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSGVGRGDFGSLAPRVARQL 20
Db .11 GSGVGRGDFGSLAPRVARQL 29
|||||
RESULT 15
AAW17087
ID AAW17087 standard; peptide: 31 AA.
AC AAW17087;
XX
DF 13-JUN-1997 (first entry)
XX
DE Foot and mouth disease virus modified G-H loop of protein VP-1.
XX
KW Foot and mouth disease; aphthovirus; vaccine; antigen; epitope;
KW Immunogen; G-H loop; VP-1; deletion; mutant; binding site removal;
KW antibody; non-infectious; attenuated.
XX
OS Foot and mouth disease virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 17 /label= substitution
FT /note= "wild-type Asp replaced with Glu"
XX
PN US5612040-A.
XX
PD 18-MAR-1997.
XX
PE 07-APR-1995; 95US-0418716.
XX
PR 07-APR-1995; 95US-0418716.
XX
PA (USDA) US SEC OF AGRIC.
XX
PI Baxt B, Bernstein A, Kang AS, Mason PW, Reider E;
XX
DR WPI; 1997-192081/17.
XX
PT Genetically modified foot-and-mouth disease virus - lacks
PT cell-binding site and is non-infectious, useful in vaccines
XX
PS Disclosure; Figure 2; 10pp; English.
XX
CC AAW17083-W17088 are peptides representing mutant versions of amino acids
CC 130-163 of wild-type foot and mouth disease (FMD) virus VP-1 structural
CC protein. The mutants were made in order to investigate the requirements
CC of this region for cell binding. The sequences are mutant versions of
CC the G-H loop, a flexible loop between the G and H beta strands of VP-1)
CC VP-1, which is the main antigenic site of VP-1 and is also involved in
CC cell binding. The FMD virus G-H loop peptide can be modified in a FMD
CC virus by deletion of the amino acid (aa) sequence
CC Gly-Val-Arg-Gly-Asp-Phe (aa 142-147) and replacing this sequence with the
CC sequence Asn-Pro. This results in the virus retaining its immunogenicity
CC but is not infectious because the cell binding site has been removed. The
CC genetically modified FMD virus is useful in vaccines against the
CC disease.
XX
SQ Sequence 31 AA;
Query Match 87.5%; Score 91; DB 18; Length 31;
Best Local Similarity 94.7%; Pred. No. 7.5e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 GSGVGRGDFGSLAPRVARQL 20
Db 11 GSGVGRGDFGSLAPRVARQL 29
|||||
Search completed: October 9, 2003, 10:14:18
Job time : 60.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 10:10:09 ; Search time 19.6667 Seconds

(without alignments)
97.799 Million cell updates/sec

Title: US-09-549-186b-7

Perfect score: 104

Sequence: 1 CGSGVRGDFGSLAPRYARQL 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 95 | 91.3 | 2332 | 1 GNNY4F | genome polypeptide |
| 2 | 67 | 64.4 | 216 | 2 A03911 | genome polypeptide |
| 3 | 50 | 48.1 | 230 | 2 A03909 | genome polypeptide |
| 4 | 50 | 48.1 | 2336 | 2 S37077 | genome polypeptide |
| 5 | 48 | 46.2 | 377 | 2 A53384 | polysialic acid ca |
| 6 | 48 | 46.2 | 377 | 2 S60758 | sial protein - Nei |
| 7 | 48 | 46.2 | 2333 | 1 GNNY2F | genome polypeptide |
| 8 | 47 | 45.2 | 351 | 2 E75631 | iron ABC transport |
| 9 | 47 | 45.2 | 365 | 2 F96017 | hypothetical prote |
| 10 | 46.5 | 44.7 | 326 | 2 D70696 | probable dtdp-gluc |
| 11 | 46 | 44.2 | 109 | 2 S61252 | genome polypeptide |
| 12 | 46 | 44.2 | 109 | 2 S61253 | genome polypeptide |
| 13 | 46 | 44.2 | 267 | 2 S30395 | ribosomal protein |
| 14 | 46 | 44.2 | 564 | 2 F90965 | hypothetical prote |
| 15 | 46 | 44.2 | 564 | 2 F85813 | hypothetical prote |
| 16 | 46 | 44.2 | 569 | 2 H64959 | probable membrane |
| 17 | 46 | 44.2 | 573 | 2 C71264 | hypothetical prote |
| 18 | 46 | 44.2 | 651 | 2 T32875 | hypothetical prote |
| 19 | 45.5 | 43.8 | 429 | 2 S45459 | TOM34 protein - ye |
| 20 | 45 | 43.3 | 303 | 2 E72463 | hypothetical prote |
| 21 | 44.5 | 42.8 | 1080 | 2 A35088 | phycobilisome link |
| 22 | 44 | 42.3 | 76 | 2 D82844 | carbon storage reg |
| 23 | 44 | 42.3 | 150 | 2 S60258 | meltrin beta - mou |
| 24 | 44 | 42.3 | 379 | 1 D59080 | Cdc6 related prote |
| 25 | 43.5 | 41.8 | 368 | 2 F72509 | probable developme |
| 26 | 43 | 41.3 | 301 | 2 T16844 | hypothetical prote |
| 27 | 43 | 41.3 | 312 | 2 A56911 | TRADD protein - hu |
| 28 | 42 | 40.4 | 58 | 2 S66328 | protein kinase AK1 |
| 29 | 42 | 40.4 | 291 | 2 T37992 | probable cricabox |

| | | | | | |
|----|----|------|------|----------|--------------------|
| 30 | 42 | 40.4 | 296 | 2 H75557 | hypothetical prote |
| 31 | 42 | 40.4 | 308 | 2 AC3604 | n-acetylglucosamin |
| 32 | 42 | 40.4 | 309 | 2 H71328 | probable flagellar |
| 33 | 42 | 40.4 | 331 | 2 E82389 | probable outer mem |
| 34 | 42 | 40.4 | 406 | 2 S40774 | ribonucleoprotein |
| 35 | 42 | 40.4 | 467 | 2 B75322 | probable oligoendo |
| 36 | 42 | 40.4 | 486 | 1 KRXL | keratin 3, type I, |
| 37 | 42 | 40.4 | 529 | 2 T23740 | hypothetical prote |
| 38 | 42 | 40.4 | 630 | 2 JC7831 | cancer-associated |
| 39 | 42 | 40.4 | 795 | 2 E86247 | receptor-like prot |
| 40 | 42 | 40.4 | 809 | 1 S60112 | transitional endop |
| 41 | 42 | 40.4 | 810 | 2 S75931 | hypothetical prote |
| 42 | 42 | 40.4 | 978 | 2 E36787 | protein T4012.5 (1 |
| 43 | 42 | 40.4 | 990 | 2 T03784 | probable receptor |
| 44 | 42 | 40.4 | 992 | 2 T05335 | hypothetical prote |
| 45 | 42 | 40.4 | 1002 | 2 T46033 | receptor protein k |

ALIGNMENTS

RESULT 1

GNNY4F

genome polypeptide - foot-and-mouth disease virus A (strain A12)

N/Contains: coat protein VP1; coat protein VP2; coat protein VP3; coat protein VP4; C

tein VPg2; genome-linked protein VPg3; nonstructural protein p20a; proteinase (EC 3.4

C/Species: Aphthovirus A (foot-and-mouth disease virus A)

C/Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999

C/Accession: A25794

R.Robertson, B.H.; Grubman, M.J.; Weddell, G.N.; Moore, D.M.; Welsh, J.D.; Fischer, T

J. Virol. 54, 651-660, 1985

A/Title: Nucleotide and amino acid sequence coding for polypeptides of foot-and-mouth

A/Reference number: A25794; MUID:85211015; PMID:2987518

A/Accession: A25794

A/Molecule type: genomic RNA

A/Residues: 1-2332 <ROB>

A/Cross-References: GB:M10975; NID:9210306; PIDN:AAA42593.1; PID:9210307

C/Superfamily: foot-and-mouth disease virus genome polypeptide

C/Keywords: coat protein; core protein; genome-linked protein; hydrolyase; nonstructur

F:1-216/Product: nonstructural protein p20a #status predicted <NP>

F:217-285/Product: coat protein VP4 #status predicted <VP4>

F:286-503/Product: coat protein VP2 #status predicted <VP2>

F:504-723/Product: coat protein VP3 #status predicted <VP3>

F:724-937/Product: coat protein VP1 #status predicted <VP1>

F:938-953/Product: core protein X #status predicted <CPX>

F:954-1107/Product: core protein p14 #status predicted <CP14>

F:1108-1425/Product: core protein p41 #status predicted <CP41>

F:1426-1578/Product: core protein p19 #status predicted <CP19>

F:1579-1601/Product: genome-linked protein VPg1 #status predicted <VG1>

F:1602-1625/Product: genome-linked protein VPg2 #status predicted <VG2>

F:1626-1649/Product: genome-linked protein VPg3 #status predicted <VG3>

F:1650-1862/Product: proteinase #status predicted <PPS>

F:1863-2332/Product: RNA-directed RNA polymerase #status predicted <RRP>

Query Match 91.3%; Score 95; DB 1; Length 2332;

Best Local Similarity 100.0%; Pred. No. 2.1e-06;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 2 GSGVRGDFGSLAPRYARQL 20
864 GSGVRGDFGSLAPRYARQL 882

RESULT 2

A03911

genome polypeptide - foot-and-mouth disease virus A (strain A24 Cruzeiro) (fragment)

N/Contains: coat protein VP1; core protein p52

C/Species: Aphthovirus A (foot-and-mouth disease virus A)

C/Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 26-Aug-1999

C/Accession: A03911

R.Makoff, A.J.; Paynter, C.A.; Rowlands, D.J.; Boothroyd, J.C.

Nucleic Acids Res. 10, 8285-8295, 1982

A/Title: Comparison of the amino acid sequence of the major immunogen from three sero

A:Reference number: A37503; MUID:83143292; PMID:6298715
A:Accession: A03911
A:Molecule type: genomic RNA
A:Residues: 1-216 <MAK>
A:Cross-references: GB:J02183; NID:g210312; PIDN:AAA2596.1; PID:g210313
C:Comment: Specific enzymatic cleavage in vivo yields mature proteins including coat protein
C:Superfamily: foot-and-mouth disease virus genome polypeptide
C:Keywords: polypeptide

Query Match 64.4%; Score 67; DB 2; Length 216;
Best Local Similarity 73.7%; Pred. No. 0.0051;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 GSGVRGDFGSLAPVARQL 20
DB 129 GSGRRGDMGSLAPVARQL 147

RESULT 3
A03909
genome polypeptide - foot-and-mouth disease virus A (strain A5) (fragment)
N:Contains: coat protein VP1; coat protein VP3; core protein p52
C:Species: Aphthovirus A (foot-and-mouth disease virus A)
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 07-Feb-1997
C:Accession: A03909
R:Beck, E.; Fell, G.; Strohmater, K.
EMBO J. 2, 555-559, 1983
A:Title: The molecular basis of the antigenic variation of foot-and-mouth disease virus
A:Reference number: A03909; MUID:84028562; PMID:6194987
A:Accession: A03909
A:Molecule type: mRNA
A:Residues: 1-230 <BEC>
A:Note: the authors translated the codon GCA for residue 114 as Val
C:Comment: Specific enzymatic cleavages in vivo yield mature proteins including the coat
C:Superfamily: foot-and-mouth disease virus genome polypeptide
C:Keywords: polypeptide

Query Match 48.1%; Score 50; DB 2; Length 230;
Best Local Similarity 57.9%; Pred. No. 2.6;
Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 2 GSGVRGDFGSLAPVARQL 20
DB 143 GSGRRGDMGSLAPVARQL 161

RESULT 4
S37077
genome polypeptide - foot-and-mouth disease virus A (strain A22/550 Azerbaijan 65)
N:Contains: coat protein VP1; coat protein VP2; coat protein VP3; coat protein VP4; core
tein VPg2; genome-linked protein VPg3; nonstructural protein p20a; proteinase (EC 3.4.-.
C:Species: Aphthovirus A (foot-and-mouth disease virus A)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C:Accession: S37077; JN0413
R:Sosnovtsev, S.V.; Onischenko, A.M.; Petrov, N.A.; Kalashnikova, T.I.; Mamaeva, N.V.; D
submitted to the EMBL Data Library, August 1993
A:Reference number: S37077
A:Accession: S37077
A:Molecule type: genomic RNA
A:Residues: 1-2336 <SOS>
A:Cross-references: EMBL:X74812; NID:g397965; PIDN:CA52812.1; PID:g397966
R:Onischenko, A.M.; Petrov, N.A.; Blinov, V.M.; Vassilenko, S.K.; Sandakchiev, L.S.; H
Biorog. Khim. 12, 416-419, 1986
A:Title: The DNA-copy primary structure for the gene of the FMDV A22 serotype VP1-protein
A:Reference number: JN0413; MUID:86186952; PMID:2421736
A:Accession: JN0413
A:Molecule type: genomic RNA
A:Residues: 702-955 <ONT>
A:Cross-references: GB:M38362; NID:g210514; PIDN:AAA2664.1; PID:g210515
C:Superfamily: foot-and-mouth disease virus genome polypeptide
C:Keywords: coat protein; core protein; genome-linked protein; hydrolase; nonstructural
F:1-217/Product: nonstructural protein p20a #status predicted <MPA>
F:218-286/Product: coat protein VP4 #status predicted <VP4>

F:287-504/Product: coat protein VP2 #status predicted <VP2>
F:505-724/Product: coat protein VP3 #status predicted <VP3>
F:725-938/Product: coat protein VP1 #status predicted <VP1>
F:939-954/Product: core protein X #status predicted <CPX>
F:955-1108/Product: core protein p14 #status predicted <C14>
F:1109-1426/Product: core protein p41 #status predicted <C41>
F:1427-1579/Product: core protein p19 #status predicted <C19>
F:1580-1602/Product: genome-linked protein VPg1 #status predicted <VG1>
F:1603-1626/Product: genome-linked protein VPg2 #status predicted <VG2>
F:1627-1650/Product: genome-linked protein VPg3 #status predicted <VG3>
F:1651-1863/Product: proteinase #status predicted <PTS>
F:1864-2333/Product: RNA-directed RNA polymerase #status predicted <RRP>

Query Match 48.1%; Score 50; DB 2; Length 2336;
Best Local Similarity 63.2%; Pred. No. 26;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 2 GSGVRGDFGSLAPVARQL 20
DB 865 GMGRRGDLPLAPVARQL 883

RESULT 5
A53384
polysialic acid capsule biosynthesis protein Synx NMB0070 [Imported] - Neisseria men
C:Species: Neisseria meningitidis
C>Date: 25-Aug-1995 #sequence_revision 25-Aug-1995 #text_change 19-Jan-2001
C:Accession: A53384; D81241
R:Swartley, J.S.; Stephens, D.S.
J. Bacteriol. 176, 1530-1534, 1994
A:Title: Identification of a genetic locus involved in the biosynthesis of N-acetyl-D
A:Reference number: A53384; MUID:94156865; PMID:8113198
A:Accession: A53384
A:Molecule type: DNA
A:Residues: 1-377 <SMA>
A:Cross-references: GB:U04328; NID:g460144; PIDN:AA17654.1; PID:g460145
R:Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen,
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.
et al.; H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignanl, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandt, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappouli, R.
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:2015755; PMID:10710307
A:Accession: D81241
A:Molecule type: DNA
A:Residues: 1-377 <TET>
A:Cross-references: GB:AE002366; GB:AE002098; NID:g7225284; PIDN:AA40537.1; PID:g722
A:Experimental source: serogroup B, strain MC58
C:Genetics: NMB0070

Query Match 46.2%; Score 48; DB 2; Length 377;
Best Local Similarity 52.9%; Pred. No. 8.8;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 GSGVRGDFGSLAPVARQL 17
DB 6 CINGRADFGKLPPLA 22

RESULT 6
S60758
siala protein - Neisseria meningitidis
C:Species: Neisseria meningitidis
C>Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 08-Oct-1999
C:Accession: S60758
R:Edwards, U.; Mueller, A.; Hammerschmidt, S.; Gerardy-Schahn, R.; Frosch, M.
Mol. Microbiol. 14, 141-149, 1994
A:Title: Molecular analysis of the biosynthesis pathway of the alpha-2,8 polysialic a
A:Reference number: S60758; MUID:95131727; PMID:7830552
A:Accession: S60758
A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: DNA
A:Residues: 1-377 <EDM>
A:Cross-references: EMBL:M55053; NID:g520732; PIDN:AAA20475.1; PID:g5207333
C:Genetics:
A:Gene: slaA

| | | | | |
|-----------------------|----------------|--------------|----------|------------|
| Query Match | 46.2% | Score 48 | DB 2 | Length 377 |
| Best Local Similarity | 52.9% | Pred. No. | 8.8 | |
| Matches 9 | Conservative 2 | Mismatches 6 | Indels 0 | Gaps 0 |

| QY | 1 | CGSGVRGDFGSLAPRVA | 17 |
|----|---|-------------------|----|
| | | : | : |
| Db | 6 | CITGTRADFGKIKPLLA | 22 |

C:Species: Aphthovirus A (foot-and-mouth disease virus A)
 C:Date: 17-Dec-1982 #sequence_revision 28-Aug-1985 #text_change 16-Jul-1999
 C:Accession: A93508; A91491; S30753
 R:Carroll, A.R.; Rowlands, D.J.; Clarke, B.E.
 Nucleic Acids Res. 12, 2461-2472, 1984
 A:Title: The complete nucleotide sequence of the RNA coding for the primary translation
 A:Reference number: A93508; MUID:84165547; PMID:6324120
 A:Accession: A93508
 A:Molecule type: genomic RNA
 A:Residues: 1-2333 <CAR>
 A:Cross-references: GB:X00429
 R:Boothroyd, J.C.; Harris, T.J.R.; Rowlands, D.J.; Lowe, P.A.
 Gene 17, 153-161, 1982
 A:Title: The nucleotide sequence of cDNA coding for the structural proteins of foot-and-
 A:Reference number: A91491; MUID:82211814; PMID:6282711
 A:Accession: A91491
 A:Molecule type: genomic RNA
 A:Residues: 115-385, 'C', 397-631, 'L', 633-1048 <BOO>
 A:Cross-references: GB:V01130; NID:961048; PIDN:CAA24361.1; PID:91335402
 R:Sanger, D.V.; Newton, S.E.; Rowlands, D.J.; Clarke, B.E.
 Nucleic Acids Res. 15, 3305-3315, 1987
 A:Title: All foot and mouth disease virus serotypes initiate protein synthesis at two se-
 A:Reference number: S30753; MUID:87203363; PMID:3033601

| | | | | | | | |
|-----------------------|-------|--------------|----|------------|---|--------|------|
| Query Match | 46.28 | Score | 48 | DB | 1 | Length | 2333 |
| Best Local Similarity | 71.48 | Pred. No. | 54 | | | | |
| Matches | 10 | Conservative | 1 | Mismatches | 3 | Indels | 0 |
| | | | | | | Gaps | 0 |

RESULT 8
E75631
Iron ABC transporter, permease protein - *Deinococcus radiodurans* (strain R1)

C:Species: Delnoccocus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: E75631
R:White, O.; Eelsen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
M.; Shen, M.; Vamathean, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zaleski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

| | | | | | |
|----|------------------------|-------|---------------|-------|-------------|
| | Query Match | 45.2% | Score 47; | DB 2; | Length 351; |
| | Best Local Similarity | 52.6% | Pred. No. 12; | | |
| | Matches | 10; | Conservative | 3; | Mismatches |
| | | | | 6; | Indels |
| | | | | 0; | Gaps |
| OY | 2 GSGVRGDFGSILAPRYARQL | 20 | | | |
| | : : | : | : | : | : |
| Dd | . 275 GAGILGFVGLLAPHRL | 293 | | | |

RESULT 9
 P96017
 hypothetical protein SMD20659 [imported] - *Sinorhizobium meliloti* (strain 1021) megap
 C:Species: *Sinorhizobium meliloti*
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C:Accession: P96017
 R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Kern
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A:Title: The complete sequence of the 1,683-kb pSYM megaplasmid from the N2-fixing e
 A:Reference number: A95842; MUID:21396508; PMID:11481431
 A:Accession: P96017
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-365 <RUB>
 A:Cross-references: GB:AL591985; PIDN:CA049806.1; PID:g15141294; GSPDB:GN00167
 A:Experimental source: Strain 1021, megaplasmid pSYMB
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubbl
 Pella, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lela
 A:Vandenberg, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,
 A:Title: The complete genome of the legume symbiont *Sinorhizobium meliloti*.
 A:Reference number: A96059; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: SMD20659
 A:Genome: plasmid
 C:Superfamily: multidrug resistance protein A; lipoyl/biotin-binding homology

| | | | | |
|-----------------------|-----------------|--------------|------|------------|
| Query Match | 45.2% | Score 47 | DB 2 | Length 365 |
| Best local similarity | 76.9% | Pred. No. 12 | | |
| Matches | 10 | Conservative | 1 | Mismatches |
| | | | 2 | Indels |
| | | | 0 | Gaps |
| QY | 5 VRGDFSLAPRYA | 17 | | |
| | | | | |
| DB | 63 VRGDTSLAPRYA | 75 | | |

RESULT 10
D70696
probable dtdp-glucose 4 - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: D70696
R:Colo, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; M01D:98295987; PMID:9634230
A:Accession: D70696
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1326 <COL>
A:Cross-references: GB:280343; GB:AL123456; NID:g3261648; PIDN:CAB02463.1; PID:g1552867
A:Experimental source: strain H37Rv
C:Genetics:
A:Gene: *epiB*
C:Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homology
F:3-314/Domain: UDPglucose 4-epimerase homology <UDP>

Query Match 44.7%; Score 46.5; DB 2; Length 326;
Best Local Similarity 57.9%; Pred. No. 13;
Matches 11; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

OY 4 GVR---GDGSLAPRVARQ 19
DB 179 GVRQKRGFGALPRVRQ 197

RESULT 11
S61252
genome polypeptide - foot-and-mouth disease virus Asia (isolate Asia I Mandya, Karnataka)
N:Alternate names: Immunogenic polypeptide
C:Species: Aphthovirus Asia (foot-and-mouth disease virus Asia)
A:Variety: isolate Asia I Mandya, Karnataka
C>Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 26-Aug-1999
C:Accession: S61252
R:Tulasiram, P.; Tyagi, M.; Suryanarayana, V.
Submitted to the EMBL Data Library, June 1995
A:Description: Antigenic variation in foot and mouth disease virus type Asia I isolates
A:Reference number: S61252
A:Accession: S61252
A:Molecule type: mRNA
A:Residues: 1-109 <TUL>
A:Cross-references: EMBL:X88856; NID:g971407; PIDN:CAA61326.1; PID:g971408
A:Experimental source: isolate Asia I Mandya, Karnataka
C:Superfamily: foot-and-mouth disease virus genome polypeptide
C:Keywords: coat protein; polypeptide; proteinase
F:1-91/Product: coat protein VP1 (fragment) #status predicted <MAT1>
F:92-107/Product: proteinase 2A #status predicted <MAT2>
F:108-109/Product: proteinase 2B (fragment) #status predicted <MAT3>

Query Match 44.2%; Score 46; DB 2; Length 109;
Best Local Similarity 60.0%; Pred. No. 5.3;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 6 RGDGSLAPRVAROL 20
DB 23 RGDMAALQRLSRQL 37

RESULT 12
S61253
genome polypeptide - foot-and-mouth disease virus Asia (isolate Asia I Nilgiri, Tamil Na
N:Alternate names: Immunogenic polypeptide
C:Species: coat protein VP1; proteinase 2A; proteinase 2B
C:Keywords: Aphthovirus Asia (foot-and-mouth disease virus Asia)
A:Variety: isolate Asia I Nilgiri, Tamil Nadu
C>Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 26-Aug-1999
C:Accession: S61253
R:Tulasiram, P.; Tyagi, M.; Suryanarayana, V.
Submitted to the EMBL Data Library, June 1995

A:Description: Antigenic variation in foot and mouth disease virus type Asia I isolat
A:Reference number: S61253
A:Accession: S61253
A:Molecule type: mRNA
A:Residues: 1-109 <TUL>
A:Cross-references: EMBL:X88857; NID:g971409; PIDN:CAA61327.1; PID:g971410
A:Experimental source: isolate Asia I Nilgiri, Tamil Nadu
C:Superfamily: foot-and-mouth disease virus genome polypeptide
C:Keywords: coat protein; polypeptide; proteinase
F:1-91/Product: coat protein VP1 (fragment) #status predicted <MAT1>
F:92-107/Product: proteinase 2A #status predicted <MAT2>
F:108-109/Product: proteinase 2B (fragment) #status predicted <MAT3>

Query Match 44.2%; Score 46; DB 2; Length 109;
Best Local Similarity 60.0%; Pred. No. 5.3;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 6 RGDGSLAPRVAROL 20
DB 23 RGDMAALQRLSRQL 37

RESULT 13
S30395
ribosomal protein S2, cytosolic - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 13-Aug-1999
C:Accession: S30395; S50325; S30396
R:Barrio, R.; del Arco, A.; Cabrera, H.; Arribas, C.
Nucleic Acids Res. 21, 351, 1993
A:Title: Cloning and analysis of the S2 ribosomal protein cDNA from Drosophila.
A:Reference number: S30395; M01D:93181212; PMID:8441641
A:Accession: S30395
A:Molecule type: mRNA
A:Residues: 1-267 <BAR>
A:Cross-references: EMBL:X69120; NID:g288083; PIDN:CAA48872.1; PID:g288084
A:Note: the authors did not translate the codon for residue 267
R:Cranton, S.E.; Laski, F.A.
Genetics 137, 1039-1048, 1994
A:Title: string of pearls Encodes Drosophila ribosomal protein S2, has minute-like ch
A:Reference number: S50325; M01D:95073591; PMID:7982558
A:Accession: S50325
A:Molecule type: mRNA
A:Residues: 118, 'GC', 21-193, 'K', 195-267 <CRA>
A:Cross-references: EMBL:U01334; NID:g430711; PIDN:AAC34198.1; PID:g515971
C:Genetics:
A:Gene: FlyBase:sop
A:Cross-references: FlyBase:FBgn0004867
C:Superfamily: Escherichia coli ribosomal protein S5
C:Keywords: protein biosynthesis; ribosome

Query Match 44.2%; Score 46; DB 2; Length 267;
Best Local Similarity 62.5%; Pred. No. 13;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 SGVRGDFGSRPPRGR 18
DB 9 SGFRGDFGSRPPRGR 24

RESULT 14
F90965
hypothetical protein ECs2654 [imported] - Escherichia coli (strain O157:H7, substrain
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: F90965
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kohara, S.; Shiba, T.; Hattori, M.; Shinegawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A:Reference number: A99629; M01D:21156231; PMID:11258796
A:Accession: F90965
A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-564 <HAY>
 A:Cross-references: GB:BA000007; PIDN:BA036117.1; PID:g13362162; GSPDB:GN00154
 A:Experimental source: strain O157:H7, substrain RIMD 0509952
 C:Genetics:
 A:Gene: ECs2694

Query Match 44.28; Score 46; DB 2; Length 564;
 Best local Similarity 80.08; Pred. No. 27;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 GVRGDFGSLA 13
 |||||
 DB 350 GVRGDFGSLIS 359

RESULT 15

F85813
 hypothetical protein Z3047 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: F85813
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: F85813
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-564 <STO>
 A:Cross-references: GB:AE005174; NID:g12516062; PIDN:AAG56970.1; GSPDB:GN00145; UWGP:Z30
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: Z3047

Query Match 44.28; Score 46; DB 2; Length 564;
 Best local Similarity 80.08; Pred. No. 27;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 GVRGDFGSLA 13
 |||||
 DB 350 GVRGDFGSLIS 359

Search completed: October 9, 2003, 10:18:40
 Job time : 21.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 10:02:54 ; Search time 10.3333 Seconds

(without alignments)
91.019 Million cell updates/sec

Title: US-09-549-186b-7

Perfect score: 104

Sequence: 1 CGSGVRGDFGSLAPVARQL 20

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 95 | 91.3 | 2332 | 1 | POLG_FMDVA |
| 2 | 67 | 64.4 | 216 | 1 | POLG_FMDVC |
| 3 | 50 | 48.1 | 230 | 1 | POLG_FMDVZ |
| 4 | 50 | 48.1 | 2336 | 1 | POLG_FMDVZ |
| 5 | 48 | 44.2 | 2333 | 1 | POLG_FMDV1 |
| 6 | 46 | 44.2 | 564 | 1 | YEDQ_ECO57 |
| 7 | 46 | 44.2 | 564 | 1 | YEDQ_ECOLI |
| 8 | 46 | 44.2 | 573 | 1 | Y930_TREPA |
| 9 | 45 | 43.8 | 429 | 1 | HRB1_YEAST |
| 10 | 44.5 | 42.8 | 1079 | 1 | APCE_FREDI |
| 11 | 44 | 42.3 | 379 | 1 | CD62_METTH |
| 12 | 44 | 42.3 | 920 | 1 | AD19_MOUSE |
| 13 | 43 | 41.3 | 312 | 1 | TRAD_HUMAN |
| 14 | 43 | 41.3 | 959 | 1 | G2D1_HUMAN |
| 15 | 42 | 40.4 | 309 | 1 | FLIH_TREPA |
| 16 | 42 | 40.4 | 328 | 1 | HXD1_HUMAN |
| 17 | 42 | 40.4 | 486 | 1 | R1C0_XENLA |
| 18 | 42 | 40.4 | 809 | 1 | CA8A_ARATH |
| 19 | 42 | 40.4 | 810 | 1 | SYFB_SYNY3 |
| 20 | 42 | 40.4 | 980 | 1 | CLV1_ARATH |
| 21 | 41.5 | 39.9 | 217 | 1 | SCDM_DROME |
| 22 | 41.5 | 39.9 | 933 | 1 | PERT_CANFA |
| 23 | 41 | 39.4 | 775 | 1 | SYFB_AOUAE |
| 24 | 41 | 39.4 | 1355 | 1 | CA21_RANCA |
| 25 | 41 | 39.4 | 5147 | 1 | FAT_DROME |
| 26 | 40.5 | 38.9 | 260 | 1 | ETFB_CLOTS |
| 27 | 40.5 | 38.9 | 387 | 1 | OMA2_NEIMC |
| 28 | 40.5 | 38.9 | 392 | 1 | OMA_NEIMC |
| 29 | 40.5 | 38.9 | 393 | 1 | OMA_NEIMC |
| 30 | 40.5 | 38.9 | 395 | 1 | OMA_NEIMC |
| 31 | 40 | 38.5 | 170 | 1 | RS9_STRCO |
| 32 | 40 | 38.5 | 231 | 1 | COT2_FUSSO |
| 33 | 40 | 38.5 | 231 | 1 | COT3_FUSSO |

| | | | | | |
|----|----|------|-----|---|-------------|
| 34 | 40 | 38.5 | 241 | 1 | PYRF_THETH |
| 35 | 40 | 38.5 | 281 | 1 | EPID_HUMAN |
| 36 | 40 | 38.5 | 281 | 1 | MS22_MOUSE |
| 37 | 40 | 38.5 | 290 | 1 | Y329_SYNY3 |
| 38 | 40 | 38.5 | 330 | 1 | PDXA_XYLEFA |
| 39 | 40 | 38.5 | 348 | 1 | ADH1_PICST |
| 40 | 40 | 38.5 | 422 | 1 | GF11_HUMAN |
| 41 | 40 | 38.5 | 602 | 1 | DM11_AERPE |
| 42 | 40 | 38.5 | 654 | 1 | YLH4_SCHPO |
| 43 | 40 | 38.5 | 678 | 1 | T2D5_MOUSE |
| 44 | 40 | 38.5 | 678 | 1 | T2D5_RAT |
| 45 | 40 | 38.5 | 814 | 1 | GUNE_CLOTH |

ALIGNMENTS

RESULT 1
POLG_FMDVA STANDARD; PRT; 2332 AA.
AC P03308; P03312; Q65038; Q65039; Q65040; Q65041; Q65042; Q65043;
AC Q65044; Q65045; Q65046; Q65047;
DI 21-JUL-1986 (Rel. 01, Created)
DI 01-JAN-1988 (Rel. 06, Last sequence update)
DI 28-FEB-2003 (Rel. 41, Last annotation update)
DE Genome polyprotein [Contains: Nonstructural protein p20a; Coat
DE proteins VP1 TO VP4; Core proteins X, P14, P41, P19; Genome-linked
DE proteins VPg1 TO VPg3; Picornain 3c (EC 3.4.22.28) (Protease 3c)
DE (P3C); RNA-directed RNA polymerase (EC 2.7.7.48)].
DE Foot-and-mouth disease virus (strain A12) (Aphthovirus A) (FMDV).
OS Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_Taxid=12114;
RN [1]
RE SEQUENCE FROM N.A.
RX MEDLINE=85211015; PubMed=2987518;
RA Robertson B.H., Grubman M.J., Weddell G.N., Moore D.M., Welsh J.D.,
RA Fischer T., Dowbenko D.J., Yansura D.G., Small B., Kleid D.G.;
RT "Nucleotide and amino acid sequence coding for polypeptides of
RT foot-and-mouth disease virus type A12.";
RT J. Virol. 54:651-660(1985).
[2]
RE SEQUENCE OF 1863-2332 FROM N.A.
RX MEDLINE=83225613; PubMed=6305004;
RA Robertson B.H., Morgan D.O., Moore D.M., Grubman M.J., Card J.,
RA Fischer T., Weddell G.N., Dowbenko D.J., Yansura D.G.;
RT "Identification of amino acid and nucleotide sequence of the
RT foot-and-mouth disease virus RNA polymerase.";
RT Virology 126:614-623(1983).
[3]
RE SEQUENCE OF 715-955 FROM N.A.
RX MEDLINE=82061853; PubMed=6272395;
RA Kleid D.G., Yansura D.G., Small B., Dowbenko D.J., Moore D.M.,
RA Grubman M.J., Mckercher P.D., Morgan D.O., Robertson B.H.,
RA Bachrach H.L.;
RT "Cloned viral protein vaccine for foot-and-mouth disease: responses
RT in cattle and swine.";
RT Science 214:1125-1129(1981).
[4]
RE CATALYTIC ACTIVITY: Selective cleavage of Glu-1-Gly bond in the
RE poliovirus polyprotein. In other picornavirus reactions Glu may be
RE substituted for Gln, and Ser or Thr for Gly.
[5]
RE CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
RE (RNA)(N).
[6]
RE SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHERAL UNITS,
RE EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
RE VP3, AND VP4.
[7]
RE -1- SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
[8]
RE -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.

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DR EMBL: M10975; AAA42593.1; -
DR EMBL: J02187; AAA42670.1; -
DR MEROPS: C03.008; -
DR InterPro: IPR004004; Call1c1_pol_hel.
DR InterPro: IPR004080; FMDV1coat.
DR InterPro: IPR001676; Rhv.
DR InterPro: IPR000605; RNA_helicase.
DR InterPro: IPR007095; RNA_pol_DS_PS.
DR InterPro: IPR001205; RNA_pol_P3D.
DR InterPro: IPR007094; RNA_pol_PSVir.
DR Pfam: PF00073; Rhv; 3.
DR Pfam: PF00680; RNA_dep_RNA_pol; 1.
DR Pfam: PF00910; RNA_helicase; 1.
DR PRINTS: PR00918; CALICIVIRUS.
DR PRINTS: PR01542; FMDV1coat.
KW Polypeptide; Coat protein; Core protein; RNA-directed RNA polymerase;
KW Transferase; Hydrolase; Thiol protease; Nonstructural protein;
KW Myristate.
FT CHAIN 1 200 NONSTRUCTURAL PROTEIN P20A.
FT CHAIN 201 285 COAT PROTEIN VP4.
FT CHAIN 286 503 COAT PROTEIN VP2.
FT CHAIN 504 723 COAT PROTEIN VP3.
FT CHAIN 724 937 COAT PROTEIN VP1.
FT CHAIN 938 953 CORE PROTEIN X.
FT CHAIN 954 1107 CORE PROTEIN P14.
FT CHAIN 1108 1425 CORE PROTEIN P41.
FT CHAIN 1426 1578 CORE PROTEIN P19.
FT CHAIN 1579 1601 GENOME-LINKED PROTEIN VPGL.
FT CHAIN 1602 1625 GENOME-LINKED PROTEIN VP2.
FT CHAIN 1626 1649 GENOME-LINKED PROTEIN VP3.
FT CHAIN 1650 1862 PROTEASE.
FT CHAIN 1863 2332 RNA-DIRECTED RNA POLYMERASE.
FT LIPID 201 201 MYRISTATE.
SQ SEQUENCE 2332 AA; 259408 MW; E877DA739CBEC6A CRC64;

Query Match 91.3%; Score 95; DB 1; Length 2332;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GSGVRGDFGSLAPVARQL 20
DB 864 GSGVRGDFGSLAPVARQL 882

RESULT 2
POLG_FMDV5 STANDARD; PRT; 216 AA.
AC P03307;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Genome polypeptide [Contains: Coat protein VP1; Core protein P52]
DE (Fragment).
OS Foot-and-mouth disease virus (strain A24 Cruzeiro) (Aphthovirus A)
OS (FMDV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12113;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83143292; PubMed=6298715;
RA Makoff A.J., Paynter C.A., Rowlands D.J., Boothroyd J.C.;
RT "Comparison of the amino acid sequence of the major immunogen from
RT three serotypes of foot and mouth disease virus.";
RT Nucleic Acids Res. 10:8283-8293(1982).
CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHERAL UNITS,
CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC VP3, AND VP4.
CC -1- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.

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DR EMBL: J02183; AAA42596.1; -
DR EMBL: A06733; CAA00589.1; -
DR PIR: A03911; A03911.
DR HSSP: Q88571; ITME.
DR InterPro: IPR004080; FMDV1coat.
DR InterPro: IPR001676; Rhv.
DR Pfam: PF00073; Rhv; 1.
DR PRINTS: PR01542; FMDV1coat.
KW Coat protein; Core protein; Polypeptide.
FT NON_TER 1 1
FT CHAIN 1 202 COAT PROTEIN VP1.
FT CHAIN 203 >216 CORE PROTEIN P52.
FT NON_TER 216 216
SQ SEQUENCE 216 AA; 23889 MW; 501659FF031A1D85 CRC64;

Query Match 64.4%; Score 67; DB 1; Length 216;
Best Local Similarity 73.7%; Pred. No. 0.0036;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 GSGVRGDFGSLAPVARQL 20
DB 129 GSGVRGDFGSLAPVARQL 147

RESULT 3
POLG_FMDV5 STANDARD; PRT; 230 AA.
AC P03307;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Genome polypeptide [Contains: Coat proteins VP3, VP1; Core protein
DE P52] (Fragment).
OS Foot-and-mouth disease virus (strain A5) (Aphthovirus A) (FMDV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12113;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84028562; PubMed=6194987;
RA Beck E., Reil G., Strommeyer K.;
RT "The molecular basis of the antigenic variation of foot-and-mouth
RT disease virus.";
RT EMO J. 2:555-559(1983).
CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHERAL UNITS,
CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC VP3, AND VP4.
CC -1- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
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DR EMBL: V01135; CAA24365.1; ALT_INIT.
DR EMBL: V01135; CAA24366.1; ALT_SEQ.
DR PIR: A03909; A03909.
DR HSSP: Q88571; ITME.
DR InterPro: IPR004080; FMDV1coat.
DR InterPro: IPR001676; Rhv.
DR Pfam: PF00073; Rhv; 1.


```

DR PRINTS: PR01542; FMDVPLICAT.
KM Coat protein; Core protein; Polyprotein.
FT NON_TER 1 1
FT CHAIN <1 4 COAT PROTEIN VP3.
FT CHAIN 5 216 COAT PROTEIN VP1.
FT CHAIN 217 >230 COAT PROTEIN P52.
FT NON_TER 230 230
SQ SEQUENCE 230 AA; 25369 MW; EA93A190F4CC1608 CRC64;

Query Match 48.1%; Score 50; DB 1; Length 230;
Best Local Similarity 57.9%; Pred. No. 1.6;
Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Oy 2 GSGVRGDFGSLAPRYAROL 20
Db 143 GSGRRGDMGSAARAAROL 161

RESULT 4
POLG_FMDVZ STANDARD; PRT; 2336 AA.
AC P49303;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Genome polyprotein [contains: Nonstructural protein P20A; Coat-
DE proteins VP1 to VP4; Core proteins X, P14, P41, P19; Genome-linked
DE proteins VP61 to VP63; Picornain 3C (EC 3.4.22.28) (Protease 3C)
DE (P3C); RNA-directed RNA polymerase (EC 2.7.7.48)].
OS Foot-and-mouth disease virus (strain A22/550 Azerbaijan 65)
OS (Aphthovirus A) (FMDV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=73481;
RN [1]
RP SEQUENCE FROM N.A.
RA Sosnovtsev S.V., Onischenko A.M., Petrov N.A., Kalashnikova T.I.,
RA Mamueva N.V., Drygin V.Y., Petrovichkova N.A., Vasilenko S.K.;
RA Submitted (Aug-1993) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Selective cleavage of Gln-1-Gly bond in the
CC poliovirus polyprotein. In other picornavirus reactions Glu may be
CC substituted for Gln, and Ser or Thr for Gly.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
CC [RNA](N).
CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHERAL UNITS,
CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC VP3, AND VP4.
CC -1- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
CC -----
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CC -----
DR EMBL: X74812; CAAS2812.1; -
DR PIR: S37077; S37077.
DR HSSP: Q88571; 1TME.
DR MEROPS: C03.008; -
DR MEROPS: C28.001; -
DR InterPro: IPR004004; Calic1_pol_hel.
DR InterPro: IPR004080; FMDVPLICAT.
DR InterPro: IPR001676; Rhv.
DR InterPro: IPR000605; RNA_helicase.
DR InterPro: IPR007095; RNA_pol_DS_PS.
DR InterPro: IPR001205; RNA_pol_P3D.
DR InterPro: IPR007094; RNA_pol_PSV1r.
DR Pfam: PF00073; rhv.3.
DR Pfam: PF00680; RNA_dep_RNA_pol.1.
DR Pfam: PF00910; RNA_helicase.1.

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DR PRINTS: PR00918; CALICVIRUSNS.
DR PRINTS: PR01542; FMDVPLICAT.
KM Polyprotein; Coat protein; Core protein; RNA-directed RNA polymerase;
KM Transferase; Hydrolase; Thiol protease; Nonstructural protein;
KM Myristate.
FT CHAIN 1 201 NONSTRUCTURAL PROTEIN P20A.
FT CHAIN 202 286 COAT PROTEIN VP4.
FT CHAIN 287 504 COAT PROTEIN VP2.
FT CHAIN 505 724 COAT PROTEIN VP3.
FT CHAIN 725 938 COAT PROTEIN VP1.
FT CHAIN 939 954 CORE PROTEIN X.
FT CHAIN 955 1108 CORE PROTEIN P14.
FT CHAIN 1109 1426 CORE PROTEIN P41.
FT CHAIN 1427 1579 CORE PROTEIN P19.
FT CHAIN 1580 1602 GENOME-LINKED PROTEIN VP61.
FT CHAIN 1603 1626 GENOME-LINKED PROTEIN VP62.
FT CHAIN 1627 1650 GENOME-LINKED PROTEIN VP63.
FT CHAIN 1651 1863 PROTEASE.
FT CHAIN 1864 2336 RNA-DIRECTED RNA POLYMERASE.
FT LIPID 202 202 MYRISTATE (BY SIMILARITY).
SQ SEQUENCE 2336 AA; 259982 MW; 15AC2AB022B5B954 CRC64;

Query Match 48.1%; Score 50; DB 1; Length 2336;
Best Local Similarity 63.2%; Pred. No. 15;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 2 GSGVRGDFGSLAPRYAROL 20
Db 865 GSGRRGDMGSAARAAROL 883

RESULT 5
POLG_FMDV1 STANDARD; PRT; 2333 AA.
AC P03306; Q64768; Q84750; Q84751; Q84752; Q84753; Q84754; Q84760;
AC Q84761; Q84762; Q84763; Q84764; Q84765; Q84766; Q84767; Q84768;
AC Q84769; Q89824;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Genome polyprotein [contains: Nonstructural protein P20A; Coat
DE proteins VP1 to VP4; Core protein P52; Genome-linked proteins VP61 to
DE VP63; Picornain 3C (EC 3.4.22.28) (Protease 3C) (P3C); RNA-directed
DE RNA polymerase P56A (EC 2.7.7.48)].
OS Foot-and-mouth disease virus (strain A10-61) (Aphthovirus A) (FMDV).
OS Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12112;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-84169547; PubMed-6324120;
RA Carroll A.R., Rowlands D.J., Clarke B.E.;
RA "The complete nucleotide sequence of the RNA coding for the primary
RA translation product of foot and mouth disease virus.";
RA Nucleic Acids Res. 12:2461-2472(1984).
RN [2]
RP SEQUENCE OF 115-1048 FROM N.A.
RX MEDLINE-82211814; PubMed-6282711;
RX Boothroyd J.C., Harris T.J.R., Rowlands D.J., Lowe P.A.;
RX "The nucleotide sequence of cDNA coding for the structural proteins
RX of foot-and-mouth disease virus.";
RL Gene 17:153-161(1982).
CC -1- CATALYTIC ACTIVITY: Selective cleavage of Gln-1-Gly bond in the
CC poliovirus polyprotein. In other picornavirus reactions Glu may be
CC substituted for Gln, and Ser or Thr for Gly.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
CC [RNA](N).
CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHERAL UNITS,
CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC VP3, AND VP4.
CC -1- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
CC -----

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DR EMBL; V01130; CAA24361.1; -;
 DR EMBL; X00429; CAA25127.1; -;
 DR MEROPS; C03.008; -;
 DR MEROPS; C28.001; -;
 DR InterPro; IPR004004; Calicet_pol_hel.
 DR InterPro; IPR004080; FMDVpcoat.
 DR InterPro; IPR001676; RV.
 DR InterPro; IPR000605; RNA_helicase.
 DR InterPro; IPR007095; RNA_pol_DS_PS.
 DR InterPro; IPR001205; RNA_pol_P3D.
 DR InterPro; IPR007094; RNA_pol_PSVir.
 DR Pfam; PF00073; Thv; 3.
 DR Pfam; PF00680; RNA_dep_RNA_pol; 1.
 DR Pfam; PF00910; RNA_helicase; 1.
 DR PRINTS; PR00918; CALICIVIRUS.
 DR PRINTS; PR01542; FMDVPCOAT.
 KM Polypeptide; Coat protein; Core protein; RNA-directed RNA polymerase;
 KM Transferase; Hydrolyase; Thiol protease; Nonstructural protein;
 KW Myristate.
 FT CHAIN 1 201
 FT CHAIN 202 286
 FT CHAIN 287 504
 FT CHAIN 505 725
 FT CHAIN 726 937
 FT CHAIN 938 1578
 FT CHAIN 1579 1601
 FT CHAIN 1602 1625
 FT CHAIN 1626 1649
 FT CHAIN 1650 1863
 FT CHAIN 1864 2333
 FT LIPID 202 202
 FT CONFLICT 396 396
 FT CONFLICT 632 632
 SQ SEQUENCE 2333 AA; 259645 MW; 4FC667DCC521BC60 CRC64;
 Query Match 46.28; Score 48; DB 1; Length 2333;
 Best Local Similarity 71.48; Pred. No. 30;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

RESULT 6
 YEDO_ECO57
 ID YEDO_ECO57 STANDARD; PRT; 564 AA.
 AC Q8XB92;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein yedo.
 GN YEDO OR 23047 OR ECS2694.
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074933; Pubmed=11206551;
 RA Perna N.T., Plunkett G., Ili, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

RA Apodaca J., Anantharaman T.S., Iin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
 RL Nature 409:529-533(2001).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / RIMD 0509952;
 RX MEDLINE=21156231; Pubmed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
 RA Kunara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
 RT O157:H7 and genomic comparison with a laboratory strain K-12.";
 RL DNA Res. 8:11-22(2001).
 CC -1 SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1 SIMILARITY: BELONGS TO THE YAC / YFIN (E.COLI), YHCK (B.SUBTILIS)
 CC FAMILY.
 CC -1 SIMILARITY: Contains 1 GGDEF domain.
 CC
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DR EMBL; AE005417; AGS56970.1; -;
 DR EMBL; AP002559; BAB36117.1; -;
 DR PIR; P90965; P90965.
 DR InterPro; IPR00160; GGDEF.
 DR Pfam; PF00990; GGDEF; 1.
 DR SMART; SM00267; DUF1; 1.
 DR TIGRFAMs; TIGR00254; GGDEF; 1.
 DR PROSITE; PS50887; GGDEF; 1.
 KM Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 20 40
 FT TRANSMEM 360 380
 FT DOMAIN 428 563
 SQ SEQUENCE 564 AA; 64287 MW; BEBC2286DABAEBC0 CRC64;
 Query Match 44.28; Score 46; DB 1; Length 564;
 Best Local Similarity 80.08; Pred. No. 15;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
 YEDO_ECOLI
 ID YEDO_ECOLI STANDARD; PRT; 564 AA.
 AC P76330; P94746;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein yedo.
 GN YEDO OR B1956.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; Pubmed=9278503;
 RA Blattner F.R., Plunkett G., Ili, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";

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RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Alpha H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasai H., Kimura S., Kitagawa M., Kitagawa M., Makino K., Miki T.,
RA Mizubuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Samped G., Seki Y.,
RA Sivaubandam S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horinouchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -1- SIMILARITY: BELONGS TO THE YAC / YFIN (E.COLI), YHCK (B.SUBTILIS)
CC FAMILY.
CC -1- SIMILARITY: Contains 1 GGDEF domain.
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CC -----
DR EMBL; AE000287; AAC75022.1; ALT_INIT.
DR EMBL; D90835; BAA15784.1; -.
DR Ecogene; EG14040; yedQ.
DR InterPro; IPR00160; GGDEF.
DR Pfam; PF00990; GGDEF.
DR SMART; SM00267; DUF1.1.
DR TIGRfams; TIGR00254; GGDEF.1.
DR PROSITE; PS50887; GGDEF.1.
DR Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 20 40 POTENTIAL.
FT TRANSMEM 360 380 POTENTIAL.
FT DOMAIN 428 563 GGDEF.
SO SEQUENCE 564 AA; 64283 MW; 05FB02C1BE2A8938 CRC64;

Query Match 44.28; Score 46; DB 1; Length 564;
Best Local Similarity 80.08; Pred. No. 15;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 GVRGDFGSLA 13
Db 350 GVRGDFGSLA 359

RESULT 8
Y930 TREPA STANDARD; PRT; 573 AA.
ID Y930 TREPA
AC 083900;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein TP0930.
GN TP0930.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetales; Spirochaetales; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Nichols;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
RA Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Soergren E., Hardson J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khaliq H., Richardson D., Howell J.K., Chidambaram M., Ueberback T.,
RA McConnel L., Artach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;

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RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete.";
RL Science 281:375-388(1998).
CC -----
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CC -----
DR EMBL; AE001261; AAC65889.1; -.
DR PIR; C71264; C71264.
DR TIGR; TP0930; -.
KW Hypothetical protein; Complete proteome.
SO SEQUENCE 573 AA; 64723 MW; 4A085F7C7B612BEA CRC64;

Query Match 44.28; Score 46; DB 1; Length 573;
Best Local Similarity 56.28; Pred. No. 16;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 GVRGDFGSLAPRYAR 18
Db 12 GVRGDFGSLAPRYAR 27

RESULT 9
HRBL YEAST STANDARD; PRT; 429 AA.
ID HRBL YEAST
AC P38922;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE HRBL protein (POM34 protein).
GN HRBL OR TOM34 OR YND004W OR N2009.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GRP88;
RX MEDLINE=94005822; PubMed=8402262;
RA Lalo D., Stettler S., Mariotte S., Slonimski P.P., Thuriaux P.;
RT "Two yeast chromosomes are related by a fossil duplication of their
RT centromeric regions.";
RL C. R. Acad. Sci., III, Sci. Vie 316:367-373(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-GRP88;
RX MEDLINE=95028151; PubMed=7941739;
RA Lalo D., Stettler S., Mariotte S., Gendreau E., Thuriaux P.;
RT "Organization of the centromeric region of chromosome XIV in
RT Saccharomyces cerevisiae.";
RL Yeast 10:523-533(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C / FY1679;
RX MEDLINE=95076713; PubMed=7985421;
RA Verhasselt P., Aert R., Voet M., Volckaert G.;
RT "Nucleotide sequence analysis of an 8887 bp region of the left arm of
RT yeast chromosome XIV, encompassing the centromere sequence.";
RL Yeast 10:945-951(1994).
CC -1- SUBCELLULAR LOCATION: Nuclear (potential).
CC -1- SIMILARITY: STRONG, TO YEAST GBP2.
CC -1- SIMILARITY: Contains 3 RNA recognition motif (RRM) domains.
CC -----
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DR EMBL: U02536; AAA64803.1; -
 DR EMBL: X77114; CAA54378.1; -
 DR EMBL: 271280; CAA35863.1; -
 DR PIR: S45459; S45459.
 DR HSSP: P09651; 1HA1.
 DR SDD: S0004949; HRB1.
 DR GO: GO:0005737; C:cytoplasm; IDA.
 DR GO: GO:0030530; C:heterogeneous nuclear ribonucleoprotein com. .; NAS.
 DR GO: GO:0006606; P:protein-nucleus import; IPI.
 DR InterPro: IPR000504; RNA_rec_mot.
 DR Pfam: PF00076; rrm; 3.
 DR SMART: SM00360; RRM; 3.
 DR PROSITE: PS00102; RRM; 3.
 DR PROSITE: PS00030; RRM_RNP_1; FALSE_NEG.
 KM RNA-Binding: Nuclear protein; Repeat.
 FT DOMAIN 136 212 RNA-BINDING (RRM) 1.
 FT DOMAIN 236 313 RNA-BINDING (RRM) 2.
 FT DOMAIN 351 428 RNA-BINDING (RRM) 3.
 SQ SEQUENCE 429 AA; 49141 MW; DCOF732EFA43EE89 CRC64;

Query Match 43.8%; Score 45.5; DB 1; Length 429;
 Best Local Similarity 55.6%; Pred. No. 14;
 Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 3 SGVRGDFGSLAPRVARQL 20
 DB 108 SGARGDYG---PLLAEL 122

RESULT 10
 ACPE_FREDI
 ID ACPE_FREDI STANDARD; PRT; 1079 AA.
 AC P16566;
 DT 01-ANG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Phycobillosome 120 kDa linker polypeptide, core (L-CM 92) (Core-membrane linker protein).
 GN APC3.
 OS Fremyella diplosiphon (Calothrix PCC 7601).
 OC Bacteria; Cyanobacteria; Nostocales; Microthetaceae; Fremyella.
 OX NCBI_TaxID=1197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90192765; PubMed=2107546;
 RA Howard J., Capuano V., Colombano M.V., Coursin T., de Marsac N.;
 RT Molecular characterization of the terminal energy acceptor of cyanobacterial phycobillosomes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:2152-2156(1990).
 CC -1- FUNCTION: THIS PROTEIN IS POSTULATED TO ACT BOTH AS TERMINAL ENERGY ACCEPTOR (BY ITS PHYCOBILLIN-LIKE DOMAINS) AND AS A LINKER POLYPEPTIDE (BY ITS REPEATS AND ARMS) THAT STABILIZES THE PHYCOBILLISOME CORE ARCHITECTURE.
 CC -1- SUBUNIT: PHYCOBILLISOMES OF THIS ORGANISM ARE COMPOSED OF A TWO CYLINDER CORE, FROM WHICH SIX RODS RADIATE. THE CORE IS MAINLY COMPOSED OF ALLOPHYCOCYANIN ALPHA AND BETA CHAINS, AND OF THREE MINOR COMPONENTS: THE ALLOPHYCOCYANIN ALPHA-B CHAIN, A 18.3 kDa POLYPEPTIDE, AND THE ANCHOR POLYPEPTIDE LCM.
 CC -1- SUBCELLULAR LOCATION: ANCHORS THE PHYCOBILLISOME PERPENDICULARLY TO THE STROMAL SURFACE OF THE THYLAKOID MEMBRANE.
 CC -1- SIMILARITY: THE REPEATED DOMAINS ARE SIMILAR TO THE N-TERMINAL REGIONS OF PHYCOCYANIN ROD LINKER POLYPEPTIDES.
 CC -1- SIMILARITY: THE PHYCOBILLIN-LIKE DOMAINS ARE SIMILAR TO PHYCOBILLINS FROM VARIOUS SPECIES.
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DR EMBL: M20806; AAA24873.1; -
 DR PIR: A35088; A35088.
 DR HSSP: P00318; 1B33.
 DR InterPro: IPR001297; PBS_Linker_poly.
 DR InterPro: IPR001659; Phycobillosome.
 DR Pfam: PF00427; PBS_Linker_poly; 4.
 DR Pfam: PF00502; Phycobillosome; 1.
 DR ProDom: PD000852; PBS_Linker_poly; 4.
 DR ProDom: PD000340; Phycobillosome; 2.
 KM Phycobillosome; Electron transport; Photosynthesis; Repeat.
 FT INIT_MET 0 0
 FT DOMAIN 17 75 PHYCOBILLIN-LIKE 1.
 FT DOMAIN 76 143 PHYCOBILLIN-LIKE LOOP.
 FT DOMAIN 144 236 PHYCOBILLIN-LIKE 2.
 FT DOMAIN 237 284 ARM 1 (SPACING SEQUENCE).
 FT REPEAT 285 409 I.
 FT REPEAT 410 546 ARM 2 (SPACING SEQUENCE).
 FT REPEAT 547 669 II.
 FT DOMAIN 670 743 ARM 3 (SPACING SEQUENCE).
 FT REPEAT 744 869 III.
 FT DOMAIN 870 953 ARM 4 (SPACING SEQUENCE).
 FT REPEAT 954 1079 IV.
 SQ SEQUENCE 1079 AA; 120325 MW; 87FE38F232BFCF82 CRC64;

Query Match 42.8%; Score 44.5; DB 1; Length 1079;
 Best Local Similarity 62.5%; Pred. No. 49;
 Matches 10; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 4 GVRGDFGSLAPRVAR 18
 DB 504 GARGEFSGIAGPKVFR 519

RESULT 11
 CD62_METTH
 ID CD62_METTH STANDARD; PRT; 379 AA.
 AC O27636;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cell division control protein 6 homolog 2 (CDC6 homolog 2).
 GN CDC6-2 OR MTH1599.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=187420;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-Delta H;
 RC MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Doucette-Stamm L.A., Delonghery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jivani N., Caruso A., Bush D., Saffer H., Patwell D., Prabhakar S., McDougall S., Shiner G., Goyal A., Pietrowski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";
 RL J. Bacteriol. 179:7135-7155(1997).
 RN [2]
 RP PHOSPHORYLATION, AND MUTAGENESIS OF LYS-71 AND ASP-149.
 RX MEDLINE=21405752; PubMed=11514535;
 RA Grabowski B., Kelman Z.;
 RT "Autophosphorylation of archaeal Cdc6 homologues is regulated by DNA.";
 RL J. Bacteriol. 183:5459-5464(2001).
 CC -1- FUNCTION: Might be involved in the initiation of DNA replication.
 CC -1- INDUCTION: Both single-stranded DNA and double-stranded DNA inhibit the phosphorylation reaction.

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CC -1- PTM: Autophosphorylated on a serine.
CC -1- SIMILARITY: BELONGS TO THE CDC6/CDC18 FAMILY.
CC -----
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CC -----
DR EMBL; AF000919; AAB86072.1; -
DR PIR; D69080; D69080.
DR PHOSITE; O27636; -.
DR HANAP; MF_01407; -.
KW DNA replication; Phosphorylation; ATP-binding; Complete proteome.
FT NP_BIND 65 72 ATP.
FT MUTAGEN 148 148 K->E. NO LABELING WITH ATP.
FT MUTAGEN 148 148 D->N. RETAINS SOME ABILITY TO BE LABELED.
SQ SEQUENCE 379 AA; 43301 MW; 48692C544BF94D01 CRC64;

Query Match 42.3%; Score 44; DB 1; Length 379;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 GSGVGRDPSGLAPRYAQ 19
DB 354 GKGVGRNGRILIPRESRE 371
ID 11111: 11111:
AD19_MOUSE STANDARD; PRT; 920 AA.
AC 035674;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE ADAM 19 precursor (PC 3.4.24.-) (A disintegrin and metalloprotease
DE domain 19) (Meltin beta).
GN ADAM19 OR MTNB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Myoblasts;
RX MEDLINE=98129833; PubMed=9461614;
RA Inoue D., Reid M.S., Lum L., Kraetzschmar J., Westkamp G., Myung Y.M.,
RA Baron R., Blobel C.P.;
RT "Cloning and initial characterization of mouse meltin beta and
RT analysis of the expression of four metalloprotease-disintegrins in
RT bone cells."
RL J. Biol. Chem. 273:4180-4187(1998).
RN [2]
RP SEQUENCE FROM N.A. AND DEVELOPMENTAL STAGE.
RC TISSUE-Myoblasts;
RX MEDLINE=98286128; PubMed=9622634;
RA Kurisaki T., Masuda A., Osumi N., Nabeshima Y.-I., Fujisawa-Sehara A.;
RT "Spatially- and temporally-restricted expression of meltin alpha
RT (ADAM12) and beta (ADAM19) in mouse embryo."
RL Mech. Dev. 73:211-215(1998).
RN [3]
RP SEQUENCE OF 429-578 FROM N.A.
RC TISSUE-Embryonic fibroblast;
RX MEDLINE=96026308; PubMed=7566181;
RA Yagami-Hitomasa T., Sato T., Kurisaki T., Kamijo K., Nabeshima Y.-I.,
RA Fujisawa-Sehara A.;
RT "A metalloprotease-disintegrin participating in myoblast fusion."
RL Nature 377:652-656(1995).
RN [4]
RP FUNCTION.
RX MEDLINE=21153759; PubMed=1116142;

RA Shitake K., Wakatsuki S., Kurisaki T., Fujisawa-Sehara A.;
RT Roles of Meltin beta/ADAM19 in the processing of neuregulin."
RL J. Biol. Chem. 276:9352-9358(2001).
CC -1- FUNCTION: PARTICIPATES IN THE PROTEOLYTIC PROCESSING OF BETA-TYPE
CC NEUREGULIN ISOFORMS WHICH ARE INVOLVED IN NEUROGENESIS AND
CC SYNAPTOGENESIS, SUGGESTING A REGULATORY ROLE IN GLIAL CELL. ALSO
CC CLEAVES ALPHA-2 MACROGLOBULIN. MAY BE INVOLVED IN OSTEOBLAST
CC DIFFERENTIATION AND/OR OSTEOBLAST ACTIVITY IN BONE (BY
CC SIMILARITY).
CC -1- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION
CC IN BONE, HEART AND LUNG, FOLLOWED BY BRAIN AND SPLEEN AND
CC RELATIVELY LOW EXPRESSION IN LIVER, SKELETAL MUSCLE, KIDNEY AND
CC TESTIS. IN BONE, PRIMARILY EXPRESSED IN CELL OF THE OSTEOBLAST
CC LINEAGE AND NOT DETECTED IN MATURE OSTEOCLASTS.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE HEART AND IN THE TAIL BUD AT
CC 8.0 DPC, AND THEN IN THE CRANIAL AND DORSAL ROOT GANGLIA. ALSO
CC EXPRESSED WEAKLY AND TRANSIENTLY IN THE INTESTINE, LUNG AND IN
CC BONE MARROW.
CC -1- INDUCTION: BY CALCITRIOL AND DURING OSTEOBLAST DIFFERENTIATION.
CC -1- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
CC SIMILARITY).
CC -1- SIMILARITY: belongs to peptidase family M12B.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -1- SIMILARITY: Contains 1 disintegrin domain.
CC -----
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CC -----
DR EMBL; AF019887; AAC0037.1; -
DR EMBL; D50410; BAA18923.2; -.
DR HSSP; P18619; IFVL.
DR MEROPS; M12.214; -.
DR MGD; MGI:105377; Adam19.
DR InterPro: IPR006586; ADAM_cysteine.
DR InterPro: IPR001762; Disintegrin.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR001818; Matrxin.
DR InterPro: IPR002870; Pep_M12B_propep.
DR InterPro: IPR001590; Reprolysin.
DR InterPro: IPR006025; Zn_MTPeptide.
DR Pfam; PF00200; disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR ProDom; PD00664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISTR; 1.
DR PROSITE; PS50215; ADAM_MEROPS; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; FALSE_NEG.
DR PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
DR PROSITE; PS00214; DISINTEGRIN_2; 1.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR HYDROLASE; Metalloprotease; zinc; Signal; Glycoprotein; zymogen;
KW Transmembrane; EGF-like domain; SH3-binding.
FT SIGNAL 1 26 POTENTIAL.
FT PROPEP 27 204 BY SIMILARITY.
FT CHAIN 205 920 ADAM 19.
FT DOMAIN 27 703 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 704 724 POTENTIAL.
FT DOMAIN 725 920 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 211 409 METALLOPROTEASE.
FT DOMAIN 417 503 DISINTEGRIN-LIKE.
FT DOMAIN 435 438 POLY-GU.
FT DOMAIN 504 653 CYS-RICH.

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FT DOMAIN 654 686 EGF-LIKE.
 FT SITE 616 621 POLY-GLU.
 FT SITE 835 841 SH3-BINDING (POTENTIAL).
 FT SITE 840 846 SH3-BINDING (POTENTIAL).
 FT SITE 133 133 CYSTEINE SWITCH (POTENTIAL).
 FT METAL 346 346 ZINC (CATALYTIC).
 FT ACT_SITE 347 347 ZINC (CATALYTIC).
 FT METAL 350 350 ZINC (CATALYTIC).
 FT METAL 356 356 ZINC (CATALYTIC).
 FT DISULFID 321 404 BY SIMILARITY.
 FT DISULFID 361 388 BY SIMILARITY.
 FT DISULFID 466 488 BY SIMILARITY.
 FT DISULFID 658 668 BY SIMILARITY.
 FT DISULFID 662 674 BY SIMILARITY.
 FT DISULFID 676 685 BY SIMILARITY.
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 649 649 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 920 AA: 100860 MW: 7094FDD4EE547382 CRC64;

Query Match 42.3%; Score 44; DB 1; Length 920;
 Best Local Similarity 38.9%; Pred. No. 50;
 Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CGSGVRGDFGSLARVAR 18
 Db 555 CGKGLNGYRCRSPDRAK 572

RESULT 13

ID TRAD_HUMAN STANDARD; PRT; 312 AA.
 AC Q15628;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor type 1 associated DEATH domain protein
 DE (TNFR1-associated DEATH domain protein) (TNFRSF1A-associated via death domain).
 GN TRAD.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95277836; PubMed=7758105;
 RA Hau H., Xiong J., Goeddel D.V.;
 RT "The TNF receptor 1-associated protein TRADD signals cell death and NF-kappa B activation.";
 RL Cell 81:495-504(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Schenkerflug C.G., Dechant M., Fellenberg J., Everbeck V.,
 RA Debatin K.M.;
 RT "Sequence, genomic organisation, and mutational analysis of the human TRADD gene in childhood B- and T-lineage acute lymphoblastic leukemia and ALPS.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueidi T.B., Toshlyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huljk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Matra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP INTERACTION WITH RIPK1.
 RX MEDLINE=96200892; PubMed=8612133;
 RA Hsu H., Huang J., Shu H.-B., Baichwal V.R., Goeddel D.V.;
 RT "TNF-dependent recruitment of the protein kinase RIP to the TNF receptor-1 signaling complex.";
 RL Immunity 4:387-396(1996).
 RN [5]
 RP STRUCTURE BY NMR OF 1-179.
 RX PubMed=10911999;
 RA Tsao D.H., McDonagh T., Telliez J.B., Hsu S., Malakian K., Xu G.Y.,
 RA Lin L.L.;
 RT "Solution structure of N-TRADD and characterization of the interaction of N-TRADD and C-TRAF2, a key step in the TNFR1 signalling pathway.";
 RL Mol. Cell 5:1051-1057(2000).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 1-179 IN COMPLEX WITH TRAF2.
 RX PubMed=10892748;
 RA Park Y.C., Ye H., Hsia C., Segal D., Rich R.L., Liou H.C.,
 RA Myszka D.G., Wu H.;
 RT "A novel mechanism of TRAF signaling revealed by structural and functional analyses of the TRADD-TRAF2 interaction.";
 RL Cell 101:777-787(2000).
 CC -1- FUNCTION: Adapter molecule for TNFRSF1A/TNFR1 that specifically associates with the cytoplasmic domain of activated TNFRSF1A/TNFR1 mediating its interaction with FADD. Overexpression of TRADD leads to two major TNF-induced responses, apoptosis and activation of NF-kappa-B.
 CC -1- SUBUNIT: Heterodimer with TNFRSF1A/TNFR1. Binds to TRAF2.
 CC -1- TISSUE SPECIFICITY: Found in all examined tissues.
 CC -1- DOMAIN: Requires the intact DEATH domain to associate with TNFRSF1A/TNFR1.
 CC -1- SIMILARITY: Contains 1 death domain.
 CC -----
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 CC -----
 CC EMBL: L41690; AAA98482.1; ALT_INIT.
 CC DR EMBL: AJ311614; CAC38018.2; -.
 CC DR EMBL: AJ311615; CAC38018.2; JOINED.
 CC DR EMBL: AJ311616; CAC38018.2; JOINED.
 CC DR EMBL: BC004491; AA04491.1; -.
 CC DR PIR: A56911; A56911.
 CC DR PDB: 1F2H; 24-MAY-00.
 CC DR PDB: 1F3V; 06-JUN-00.
 CC DR Genew: HGNC:12030; TRADD.
 CC MIM: 603500; -.
 CC GO: GO:0006917; P:Induction of apoptosis; TAS.
 CC GO: GO:0007165; P:Signal transduction; TAS.
 CC Interpro: IPR000488; Death.
 CC DR Pfam: PF00531; death; 1.
 CC DR SMART: SM00005; death; 1.
 CC DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 CC KW Apoptosis; 3D-structure.
 CC FT DOMAIN 179 289 DEATH.

FT DOMAIN 192 198 POLY-PRO.
 SQ SEQUENCE 312 AA: 34247 MW: 5645D/E635F05A CRC64;
 Query Match 41.3%; Score 43; DB 1; Length 312;
 Best Local Similarity 61.5%; Pred. No. 25;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGSGVRGDPGSLA 13
 |||||
 DB 164 CGSGARGGDGEVA 176

RESULT 14
 G2D1_HUMAN STANDARD; PRT; 959 AA.
 AC 09UHL9: 095444; 08WVC4: 09UHK8: 09U191;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE General transcription factor II-I repeat domain-containing protein 1
 DE (GTF2I repeat domain containing protein 1) (Muscle TFII-I repeat
 DE domain-containing protein 1) (General transcription factor III) (Slow-
 DE muscle-fiber enhancer binding protein) (USE BI binding protein)
 DE (MUSTR1/BN) (Williams-Beuren syndrome chromosome region 11 protein).
 GN GTF2IR1 OR MUSTR1 OR GTF3 OR CREM1 OR RBP2 OR WBSR11 OR WBSR12.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Muscle;
 RX MEDLINE=98449952; PubMed=9774679;
 RA O'Mahoney J.V., Given K.L., Lin J., Joya J.E., Robinson C.S.,
 RA Wade R.P., Hardeman E.C.;
 RT "Identification of a novel slow-muscle-fiber enhancer binding protein,
 RT MUSTR1.";
 RL Mol. Cell. Biol. 18:6641-6652(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Colon carcinoma;
 RX MEDLINE=99216421; PubMed=10198167;
 RA Osborne L.R., Campbell T., Dardich A., Scherer S.W., Tsui L.-C.;
 RT "Identification of a putative transcription factor gene (WBSR11) that
 RT is commonly deleted in Williams-Beuren syndrome.";
 RL Genomics 57:279-284(1999).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Fetal brain;
 RX MEDLINE=20037629; PubMed=10573005;
 RA Tassabehji M., Carrette M., Wilmut C., Donat D., Read A.P.,
 RA Metcalfe K.;
 RT "A transcription factor involved in skeletal muscle gene expression is
 RT deleted in patients with Williams syndrome.";
 RL Eur. J. Hum. Genet. 7:737-747(1999).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=20044629; PubMed=10575229;
 RA Franke Y., Peoples R.J., Francke U.;
 RT "Identification of GTF2IR1, a putative transcription factor within
 RT the Williams-Beuren syndrome deletion at 7q11.23.";
 RL Cytogenet. Cell Genet. 86:296-304(1999).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1), INTERACTION WITH RBL AND MUTAGENESIS.
 RC TISSUE=Cervical carcinoma, fetal spleen, and placenta;
 RX MEDLINE=20115113; PubMed=10642537;
 RA Yan X., Zhao X., Qian M., Guo N., Gong X., Zhu X.;
 RT "Characterization and gene structure of a novel retinoblastoma-
 RT protein-associated protein similar to the transcription regulator
 RT TFII-I.";
 RL Biochem. J. 345:749-757(2000).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=uterus;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scherter C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Casavant T.L., Scheetz T.E.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Cabavut T.L., Scherter T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP FUNCTION.
 RX MEDLINE=21332325; PubMed=11438732;
 RA Tussie-Luna M.I., Bayarsaiban D., Ruddle F.H., Roy A.L.;
 RT "Repression of TFII-I-dependent transcription by nuclear exclusion.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7789-7794(2001).
 CC -1- FUNCTION: May be a transcription regulator involved in cell-cycle
 CC progression and skeletal muscle differentiation. May repress GTF2I
 CC transcriptional functions, by preventing its nuclear residency, or
 CC by inhibiting its transcriptional activation. May contribute to
 CC slow-twitch fiber type specifically during myogenesis and in
 CC regenerating muscles. Binds tropomyosin I slow-muscle fiber enhancer
 CC (USE BI). Binds specifically and with high affinity to the ERG
 CC sequences derived from the early enhancer of HOXC8 (by
 CC similarity).
 CC -1- SUBUNIT: Interacts with the retinoblastoma protein (Rb1) via its
 CC C-terminus.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9UHL9-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9UHL9-2; Sequence=VSP_003873;
 CC -1- TISSUE SPECIFICITY: Highly expressed in adult skeletal muscle,
 CC heart, fibroblast, bone and fetal tissues. Expressed at lower
 CC levels in all other tissues tested.
 CC -1- DEVELOPMENTAL STAGE: Highly expressed in developing and
 CC regenerating muscles, at the time of myofiber diversification.
 CC -1- DOMAIN: The N-terminal half may have an activating activity.
 CC -1- DISASE: Haploinsufficiency of GTF2IR1 may be the cause of
 CC certain cardiovascular and musculo-skeletal abnormalities observed
 CC in Williams-Beuren syndrome (WBS), a rare developmental disorder.
 CC It is a contiguous gene deletion syndrome involving genes from
 CC chromosome band 7q11.23.
 CC -1- SIMILARITY: BELONGS TO THE TFII-I FAMILY.
 CC -1- SIMILARITY: Contains 5 GTF2I-like repeats.
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; AF118270; AAD14687.2; -
 CC EMBL; AF1104923; AAD27668.1; -
 CC EMBL; AF151354; AAF19786.1; -
 CC EMBL; AF156489; AAF17358.1; -
 CC EMBL; AF089107; AAF21796.1; -

DR EMBL: BC018136; AAH18136.1; -
 DR GenBank: HGNC:4661; GTF21RD1.
 DR MIM: 604318; -
 DR MIM: 194050; -
 DR GO: GO:0005634; C:nucleus; NAS.
 DR GO: GO:0003705; F:RNA polymerase II transcription factor acti...; NAS.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
 DR InterPro: IPR004212; GTF21.
 DR Pfam: PF02946; GTF21; 5.
 KW Transcription regulation; Developmental protein; DNA-binding;
 KW Nuclear protein; Repeat; Alternative splicing; Polymorphism;
 KW Williams-Beuren syndrome.
 KW REPEAT 128 203 GTF21 1.
 FT REPEAT 351 426 GTF21 2.
 FT REPEAT 565 640 GTF21 3.
 FT REPEAT 705 780 GTF21 4.
 FT REPEAT 802 877 GTF21 5.
 FT DOMAIN 898 905 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 906 930 SER-RICH.
 FT VARSPLIC 656 670 Missing (in isoform 2).
 FT VARIANT 652 652 /FTid-VSP_003873.
 FT MUTAGEN 898 959 M -> V (in dbSNP:2301895).
 FT CONFLICT 111 111 /FTid-VAR_013446.
 FT CONFLICT 378 378 MISSING: CYTOPLASMIC LOCALIZATION.
 FT CONFLICT 378 378 G -> S (in REF. 1 AND 2).
 FT CONFLICT 378 378 R -> Q (in REF. 5).
 SQ SEQUENCE 959 AA: 106057 MW: 7DA3097879701340 CRC64:

Query Match 41.3%; Score 43; DB 1; Length 959;
 Best Local Similarity 50.0%; Pred. No. 75;
 Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 CGSGVRGDFGSLAP 14
 DB 480 CGPSTGELGGLRP 493

RESULT 15
 FLIH_TREPA STANDARD: PRT: 309 AA.
 AC 083416;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Flagellar assembly protein flih.
 GN FLIH OR TP0401.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=160;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Nichols;
 RX MEDLINE=96332770; PubMed=9665876;
 RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
 RA Dodson R., Gwin R., Hickey E.K., Clayton R., Ketchum K.A.,
 RA Sodergren E., Hardson J.M., McLeod M.P., Salzberg S., Peterson J.,
 RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
 RA McDonald L., Artach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
 RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 RA Venter J.C.;
 RT "Complete genome sequence of Treponema pallidum, the syphilis
 RT spirochete.";
 RL Science 281:375-388(1998).
 CC -1- FUNCTION: NEEDED FOR FLAGELLAR REGROWTH AND ASSEMBLY (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: TO FLIH IN OTHER BACTERIA AND ALSO TO FLIH.
 CC -----
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 CC -----
 DR EMBL: AE001218; AAC65389.1; -
 DR PIR: H71328; H71328.
 DR TIGR: TP0401; -
 DR InterPro: IPR000563; Flag_FLIH.
 DR Pfam: PF02108; FLIH; 1.
 KW Flagella; Complete proteome.
 SQ SEQUENCE 309 AA: 35339 MW: 213978124489C81F CRC64:

Query Match 40.4%; Score 42; DB 1; Length 309;
 Best Local Similarity 52.6%; Pred. No. 35;
 Matches 10; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 2 GSGVRGDFGSLAPRYARQL 20
 DB 267 GCVETDGEIDARVASQL 285

Search completed: October 9, 2003, 10:14:57
 Job time: 12.333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 10:09:40 : Search time 49.3333 Seconds
(without alignments)
104.616 Million cell updates/sec

Title: US-09-549-186b-7

Perfect score: 104
Sequence: 1 GSGVARGDPSLAIPYARQL 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_23: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mmc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_rvirus: *
16: sp_bacteriaph: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 71 | 68.3 | 213 | 12 | 0912L2 |
| 2 | 71 | 68.3 | 213 | 12 | 067446 |
| 3 | 71 | 68.3 | 213 | 12 | 067448 |
| 4 | 71 | 68.3 | 213 | 12 | 065093 |
| 5 | 70 | 67.3 | 20 | 12 | 09PXE4 |
| 6 | 68 | 65.4 | 213 | 12 | 098VZ6 |
| 7 | 67 | 64.4 | 210 | 12 | 067438 |
| 8 | 67 | 64.4 | 969 | 12 | 09Q2N6 |
| 9 | 66 | 63.5 | 169 | 12 | 067442 |
| 10 | 65 | 62.5 | 126 | 12 | 08V443 |
| 11 | 62 | 59.6 | 143 | 12 | 09YPU0 |
| 12 | 62 | 59.6 | 208 | 12 | 08JUR8 |
| 13 | 62 | 59.6 | 211 | 12 | 08JUP0 |
| 14 | 62 | 59.6 | 212 | 12 | 08JUP1 |
| 15 | 62 | 59.6 | 213 | 12 | 08JUS6 |
| 16 | 62 | 59.6 | 213 | 12 | 08JUM1 |

| | | | | | |
|----|----|------|-----|----|--------|
| 17 | 62 | 59.6 | 213 | 12 | 08JUP9 |
| 18 | 62 | 59.6 | 213 | 12 | 08JUP7 |
| 19 | 62 | 59.6 | 213 | 12 | 08JUP4 |
| 20 | 62 | 59.6 | 213 | 12 | 0912L1 |
| 21 | 62 | 59.6 | 213 | 12 | 08JUP5 |
| 22 | 62 | 59.6 | 213 | 12 | 08JUL1 |
| 23 | 62 | 59.6 | 213 | 12 | 08JUM1 |
| 24 | 62 | 59.6 | 213 | 12 | 08JUP5 |
| 25 | 62 | 59.6 | 213 | 12 | 08JUN0 |
| 26 | 62 | 59.6 | 213 | 12 | 08JUP3 |
| 27 | 62 | 59.6 | 213 | 12 | 08JUP2 |
| 28 | 62 | 59.6 | 213 | 12 | 08JUP1 |
| 29 | 62 | 59.6 | 213 | 12 | 08JUL0 |
| 30 | 62 | 59.6 | 213 | 12 | 08JUS7 |
| 31 | 62 | 59.6 | 213 | 12 | 08JUM0 |
| 32 | 62 | 59.6 | 213 | 12 | 08JUM3 |
| 33 | 62 | 59.6 | 213 | 12 | 08JUM8 |
| 34 | 62 | 59.6 | 213 | 12 | 08JUN9 |
| 35 | 62 | 59.6 | 213 | 12 | 08JUR0 |
| 36 | 62 | 59.6 | 213 | 12 | 08JUS5 |
| 37 | 60 | 57.7 | 197 | 12 | 08JUT2 |
| 38 | 60 | 57.7 | 213 | 12 | 08JUN4 |
| 39 | 60 | 57.7 | 652 | 12 | 09Q2N8 |
| 40 | 59 | 56.7 | 125 | 12 | 08V442 |
| 41 | 59 | 56.7 | 213 | 12 | 08JUM9 |
| 42 | 59 | 56.7 | 213 | 12 | 0912K6 |
| 43 | 59 | 56.7 | 213 | 12 | 066924 |
| 44 | 59 | 56.7 | 213 | 12 | 0912K4 |
| 45 | 59 | 56.7 | 213 | 12 | 0912L0 |

ALIGNMENTS

RESULT 1

0912L2 ID 0912L2 PRELIMINARY; PRT; 213 AA.
AC 0912L2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE VP1 protein (Fragment).
GN ID.
OS Foot-and-mouth disease virus A.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12111;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A Arg/68;
RX MEDLINE=21580796; PubMed=11724271;
RA Konig G.A., Blanco C., Knowles N.J., Palma E.L., Maradeti E.,
RA Piccone M.E.;
RT "Phylogenetic analysis of foot-and-mouth disease viruses isolated in
RT Argentina.";
RL Virus Genes 23:175-182(2001).
DR EMBL: AJ308694; CAC48168.1;
DR InterPro: IPR004080; FMDVPLcoat.
DR InterPro: IPR001676; RVH.
DR Pfam: PF00073; RVH.1.
DR PRINTS: PRO1542; FMDVPLcoat.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 213 AA; 23468 MW; 203ERCBBAB45EECE CRC64;

Query Match 68.3%; Score 71; DB 12; Length 213;
Best Local Similarity 78.9%; Pred. No. 0.0023;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GSGVARGDPSLAIPYARQL 20
DB 140 GSGRRGDMGSLAIPYARQL 158

| RESULT 2 | ID | Q67446 | PRELIMINARY; | PRT; | 213 AA. |
|----------|--|---|------------------|--------|---------|
| DT | Q67446 | 067447; | | | |
| DC | 01-NOV-1996 | (TREMBLrel, 01, Created) | | | |
| DT | 01-NOV-1996 | (TREMBLrel, 01, Last sequence update) | | | |
| DT | 01-MAR-2003 | (TREMBLrel, 23, Last annotation update) | | | |
| DE | Foot and mouth disease virus (Serotype Aven6), capsid protein VP1 mRNA (Fragment) | | | | |
| OS | Foot-and-mouth disease virus. | | | | |
| OC | Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Aphthovirus. | | | | |
| OX | NCBI_TaxID=12110; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE=65190547; PubMed=2986125; | | | | |
| RA | Weddell G.N., Yansura D.G., Dowdenko D.J., Hoatlin M.E., Grubman M.J., | | | | |
| RA | Moore D.M., Kleid D.G.; | | | | |
| RT | "Sequence variation in the gene for the immunogenetic capsid protein VP1 | | | | |
| RT | of foot-and-mouth disease virus type A."; | | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 82:2618-2622(1985). | | | | |
| DR | EMBL; K03344; AAA42600.1; .. | | | | |
| DR | InterPro; IPR004080; FMDVPIcoat. | | | | |
| DR | InterPro; IPR001676; Rnv. | | | | |
| DR | Pfam; PF00073; rnv. 1. | | | | |
| DR | PRINTS; PR01542; FMDVPIcoat. | | | | |
| FT | NON_TER | 1 | | | |
| FT | | 1 | | | |
| FT | | 213 | | | |
| SEQUENCE | 213 AA; | 23311 MW; | C4ED4E0116A0DB8A | CRC64; | |

| | | | | | | | | | | | | | | |
|--------------------------|-------|-------------------|-----------|-------------|----|----|----|----|---|---|---|---|-----|----|
| Query Match | 68.3% | Score 71; | DB 12; | Length 213; | | | | | | | | | | |
| Best Local Similarity | 78.9% | Pred. No. 0.0023; | | | | | | | | | | | | |
| Matches 15; Conservative | 1; | Mismatches 3; | Indels 0; | Gaps 0. | | | | | | | | | | |
| QY | 2 | GS | GV | RG | DF | GS | LA | PR | Y | A | R | O | L | 20 |
| | | | | | | | | | | | | | | |
| DB | 140 | GS | GR | GD | MS | LA | AR | Y | A | R | O | L | 158 | |

| RESULT 3 | ID | Q67448 | PRELIMINARY; | PTG; | 213 AA. |
|----------|--|---|--------------|------------------|---------|
| AC | Q67448; | Q67449; | | | |
| DT | 01-NOV-1996 | (TREMBLrel. 01, Created) | | | |
| DT | 01-NOV-1996 | (TREMBLrel. 01, Last sequence update) | | | |
| DE | 01-MAR-2003 | (TREMBLrel. 23, Last annotation update) | | | |
| DE | Foot and mouth disease virus (Serotype Aarg/9), capsid protein VP1 mRNA (Fragment). | | | | |
| OS | Foot-and-mouth disease virus. | | | | |
| OC | Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Aphthovirus. | | | | |
| OX | NCBI_TaxID=12110; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE=85190547; PubMed=2986125; | | | | |
| RA | Weddell G.N., Yansura D.G., Dowdenko D.J., Hoatlin M.E., Grubman M.J., Moore D.M., Kleid D.G.; | | | | |
| RT | *Sequence variation in the gene for the immunogenic capsid protein VP1 of foot-and-mouth disease virus type A.*; | | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 82:2618-2622(1985). | | | | |
| DR | EMBL; K03345; AAA42601.1; - | | | | |
| DR | InterPro: IPR004080; FMDVPIcoat. | | | | |
| DR | InterPro: IPR001676; Rhv. | | | | |
| DR | Pfam; PF00073; Rhv. 1. | | | | |
| FT | NON_TER | 1 | | | |
| FT | NON_TER | 1 | | | |
| SO | SEQUENCE | 213 AA; | 23345 MM; | 546C7FF78CD45CC0 | CRC64; |

| | | | | |
|-----------------------|-----------------|-------------------|-----------|-------------|
| Query Match | 68.3%; | Score 71; | DB 12; | Length 213; |
| Best Local Similarity | 78.9%; | Pred. No. 0.0023; | | |
| Matches 15; | Conservative 1; | Mismatches 3; | Indels 0; | Gaps 0; |

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Qy      2 GSGVRGDFGSLAPVARQQL 20
         ||| ||| ||| |||: ||
Db     140 GSGRGGDMGSLARVAQQL 158

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| RESULT 4 | | | |
|----------|---|--------------|--------------|
| 065093 | | | |
| ID | Q65093 | PRELIMINARY: | PRT: 213 AA. |
| AC | Q65093; | | |
| DT | 01-NOV-1996 (TREMBLrel. 01, Created) | | |
| DT | 01-NOV-1996 (TREMBLrel. 01, Last sequence update) | | |
| DT | 01-MAR-2003 (TREMBLrel. 23, Last annotation update) | | |
| DE | Foot and mouth disease virus strain A Venceslau VPI (Fragment). | | |
| OS | Foot-and-mouth disease virus. | | |
| OC | Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; | | |
| OC | Aphthovirus. | | |
| OX | NCBI_TaxID:12110; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RX | MEDLINE-85077620; PubMed-5096217; | | |
| RA | Cheung A., Whitehead P., Weiss S., Kupper H.; | | |
| RT | "Nucleotide sequence of the VPI gene of the foot-and-mouth disease | | |
| RT | virus strain A Venceslau."; | | |
| RL | Gene 30:241-245(1984). | | |
| DR | EMBL, M12905; AAA4263.1; - | | |
| DR | InterPro: IPR004080; FMDVPIcoat. | | |
| DR | InterPro: IPR001676; Rnv. | | |
| DR | Pfam: PF00073; rhv. 1. | | |
| DR | PRINTS: PR01542; FMDVPIcoat. | | |
| FT | NON_TER 1 | | |
| FT | NON_TER 1 | | |
| FT | NON_TER 213 | | |
| FT | NON_TER 213 | | |
| SO | SEQUENCE 213 AA; 23327 MW; 0480889571D7073 CRC64; | | |

| | Query Match | Similarity | Score 71: | DB 12: | Length 213; |
|------------|------------------|---------------------|-------------------|--------|-------------|
| Best Local | Similarity | 78.9%; | Pred. No. 0.0023; | | |
| Matches | 15; Conservative | 1; | Mismatches | 3; | Indels |
| | | | | 0; | Gaps |
| QY | 2 | GSQVGRDGFSLAPRYARQL | 20 | | |
| | | | | | |
| DB | 140 | GSQGRDGDGSLAPRYARQL | 158 | | |

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RESULT 5
09PXE4
ID 09PXE4 PRELIMINARY; PRT; 20 AA.
AC 09PXE4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE Vp1 protein (Fragment).
OS Foot-and-mouth disease virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OC NCBI_TaxID=12110;
RN [1]
RP
R2 SEQUENCE FROM N.A.
RX MEDLINE=96100820; PubMed=7483796;
RA Piatti P., Hassard S., Newman J.F., Brown F.;
RT "Antigenic variants in a plaque-isolate of foot-and-mouth disease
RL virus: implications for vaccine production.";
R3 vaccine.13:781-784(1995).
SQ SEQUENCE 20 AA; 1925 MW; E91PF87C99C19D7DB CRC64;

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| | | | | |
|-----------------------|-------|---------------------|--------|---------------|
| Query Match | 67.3% | Score 70; | DB 12; | length 20; |
| Best Local Similarity | 84.2% | Pred. No. 0.00026; | | |
| Matches | 16; | Conservative | 0; | Mismatches 3; |
| | | | Indels | 0; |
| | | | Gaps | 0; |
| QY | 2 | GSGVGRDGFSLAPRYAROL | 20 | |
| | | | | |
| DB | 1 | GSGVGRDGSGLALRYARGL | 19 | |

| RESULT 6 | 098VZ6 | PRELIMINARY; | PRT; | 213 AA. |
|-----------------------|---|--------------|-------------------|------------------------|
| ID | Q98VZ6 | | | |
| AC | Q98VZ6; | | | |
| DT | 01-JUN-2001 (TREMBLrel. 17, Created) | | | |
| DT | 01-JUN-2001 (TREMBLrel. 17, Last sequence update) | | | |
| DT | 01-MAR-2003 (TREMBLrel. 23, Last annotation update) | | | |
| DE | VPI (Fragment). | | | |
| GN | ID. | | | |
| OS | Foot-and-mouth disease virus A. | | | |
| OC | Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; | | | |
| OC | Apthovirus | | | |
| OX | NCBI_TaxID=12111; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=A76/Argentina/76; | | | |
| RX | MEDLINE=21580796; PubMed=11724271; | | | |
| RA | Kronig G.A., Blanco C., Knowles N.J., Palma E.L., Maradeti E., | | | |
| RA | Piccione M.E.; | | | |
| RT | "Phylogenetic analysis of foot-and-mouth disease viruses isolated in | | | |
| RL | Argentina."; | | | |
| DR | EMBL: AJ409219; CAC34727.1; -. | | | |
| DR | HSPD; Q88571.1; IYRE. | | | |
| DR | InterPro; IPR004080; FMDVPIcoat. | | | |
| DR | InterPro; IPR001676; Rlv. | | | |
| DR | Pfam; PF00073; rhv; 1. | | | |
| DR | PRINTS; PRO1542; FMDVPIcoat. | | | |
| FT | NON_TER | 1 | 1 | |
| FT | NON_TER | 213 | 213 | |
| SQ | SEQUENCE | 213 AA; | 23494 MM; | 92CBE4DBC85F3C9 CRC64; |
| Query Match | | 65.4%; | Score 68; | DB 12; |
| Best Local Similarity | | 78.9%; | Pred. No. 0.0071; | Length 213; |
| Matches | 15; | Conservative | 0; | Mismatches |
| | | | 4; | Indels |
| | | | 0; | Gaps |
| | | | 0; | |

| | | | |
|---|--|--|-----------------------------------|
| OY | 2 | GGSGRGDFGSLAPRVAROL | 20 |
| | | | |
| Db | 140 | GSARRGDMGSLARVAROL | 158 |
| RESULT 7 | | | |
| | 067438 | | |
| ID | 067438 | PRELIMINARY; | PRT; 210 AA. |
| AC | 067438; | | |
| DT | 01-NOV-1996 | (TReMBrel, 01, Created) | |
| DT | 01-NOV-1996 | (TReMBrel, 03, Last sequence update) | |
| DT | 01-MAR-2003 | (TReMBrel, 21, Last annotation update) | |
| DE | Foot and mouth disease virus (serotype A24), capsid protein VP1 mRNA (fragment). | | |
| OS | Foot-and-mouth disease virus. | | |
| OC | Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Aphthovirus. | | |
| OC | NCBI_TaxID=12110; | | |
| OX | [1] | | |
| RN | | | |
| RP | SEQUENCE FROM N.A. | | |
| RX | MEDLINE=85190547; PubMed=2986125; | | |
| RA | Weddell G.N., Yansura D.G., Dowbenko D.J., Hoatlin M.E., Grubman M.J., | | |
| RA | Moore D.M., Kleid D.G.; | | |
| RT | "Sequence variation in the gene for the immunogenic capsid protein VP1 of foot-and-mouth disease virus type A."; | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 82:2618-2622(1985). | | |
| DR | EMBL; K03340; AAA42595.1; " | | |
| DR | InterPro; IPR004080; FMDVPLcoat. | | |
| DR | InterPro; IPR001676; Rhv. | | |
| DR | Pfam; PF00073; rhv, 1 | | |
| DR | PRINTS; PR01542; FMDVPLCOAT. | | |
| FT | NON_TER | 1 | |
| FT | NON_TER | 1 | |
| FT | 210 | 210 | |
| SO | SEQUENCE | 210 AA; | 23089 MW; 1C96CA1C5E4F6A60 CRC64; |
| Query Match 64.4%; Score 67; DB 12; Length 210; | | | |
| Best Local Similarity 73.7%; Pzed. No. 0.01; | | | |

| | Matches | 14: Conservative | 1: Mismatches | 4: Indels | 0: Gaps | 0: |
|----------|--|----------------------|---------------|-----------|---------|----|
| QY | 2 | GSQVGRGDEGSLAPVARQQL | 20 | | | |
| | | | | | | |
| Db | 137 | GSQGRGDMGSLARVVKQL | 155 | | | |
| RESULT 8 | | | | | | |
| Q9Q2N6 | ID | Q9Q2N6 | PRELIMINARY: | PRT: | 969 AA. | |
| AC | Q9Q2N6; | | | | | |
| DT | 01-MAY-2000 (TREMBLrel. 13, Created) | | | | | |
| DT | 01-MAY-2000 (TREMBLrel. 13, Last sequence update) | | | | | |
| DT | 01-MAR-2003 (TREMBLrel. 23, Last annotation update) | | | | | |
| DE | Polyprotein (Fragment). | | | | | |
| OS | Foot-and-mouth disease virus A. | | | | | |
| OC | Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; | | | | | |
| OC | Aphthovirus. | | | | | |
| OX | NCBI_Taxid=12111; | | | | | |
| NN | [1] | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | |
| RC | STRAIN=A24/Cruzeldro/Brazil/55; | | | | | |
| RA | Abrams C.C.; | | | | | |
| RT | "Nucleotide sequence of foot-and-mouth disease virus A24/Cruzeldro/Brazil/55 from the poly(C) tract to 2B."; | | | | | |
| RU | Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases. | | | | | |

| | |
|---|---|
| RP | SEQUENCE FROM N.A. |
| RC | STRAIN-A24/Cruzneiro/Brazil/55: |
| RA | Knowles N.J., Samuel A.R., Aktas S., Rowe C.A., Abrams C.C., |
| RA | Newman J.W.I., King A.M.Q.; |
| RT | "Phylogenetic comparison of the capsid-coding region of all seven |
| RT | foot-and-mouth disease virus serotypes." |
| RL | Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases. |
| DR | HML; AJ251476; CAB62583.1; -. |
| DR | HSSP; O88571; IMME. |
| DR | MEROPS; G28_001; -. |
| DR | InterPro: IPR004080; FMDVPLcoat. |
| DR | InterPro: IPR001676; RHv. |
| DR | Pfam: PF00073; Fhv; 3. |
| DR | PRINTS; PRO1542; FMDVPLCOAT. |
| FT | CHAIN 1 >201 LEADER. |
| FT | CHAIN 202 >286 1A (VP4). |
| FT | CHAIN 287 >504 1B (VP2). |
| FT | CHAIN 505 >725 1C (VP3). |
| FT | CHAIN 726 >938 1D (VP1). |
| FT | CHAIN 939 >934 ZA. |
| FT | CHAIN 955 >969 ZB. |
| FT | NON_TER 969 969 |
| SQ | SEQUENCE 969 AA; 107629 MW; 7DD5D908FCFF89FD CRC64; |
| Query Match 64.4% Score 67; DB 12; Length 969; | |
| Best local similarity 73.7%; Pred. No. 0.053; | |
| Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0; | |
| OY | 2 GSGVRGDPGSLAPVARQL 20 : Db 865 GSGRRGMGSILARVKQL 883 |
| RESULT 9 | |
| ID | 067442 PRELIMINARY; PRT; 169 AA. |
| AC | 067442; 067443; |
| DT | 01-NOV-1996 (TREMBLrel. 01, Created) |
| DT | 01-NOV-1996 (TREMBLrel. 01, Last sequence update) |
| DT | 01-MAR-2003 (TREMBLrel. 23, Last annotation update) |
| DE | Foot and mouth disease virus (Serotype A32), capsid protein VP1 mRNA (Fragment). |
| OS | Foot-and-mouth disease virus. |
| CC | Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; |
| NC | Aphthovirus. |
| OX | NCBI_TaxID=12110; |

```
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85190547; PubMed=2986125;
RA Wedge D.M., Kleid D.G., Dowbenko D.J., Hostlin M.E., Grubman M.J.,
MOORE D.M., Kleid D.G.;
RT "Sequence variation in the gene for the immunogenic capsid protein VP1
of foot-and-mouth disease virus type A."
RL Proc. Natl. Acad. Sci. U.S.A. 82:2618-2622(1985).
DR HSSP; K03342; AAA42598.1; -.
DR InterPro; IPR004080; FMDVp1coat.
DR InterPro; IPR001676; Rhv.
DR Pfam; PF00073; rhv; 1.
DR PRINTS; PR01542; FMDVp1coat.
FT NON_TER 1 1
FT NON_TER 169 169
SQ SEQUENCE 169 AA; 18499 MW; 9E8ADC94AC57F67 CRC64;

Query Match 63.5%; Score 66; DB 12; Length 169;
Best Local Similarity 73.7%; Pred. No. 0.012;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 GSGVGDGSLAPRYARQL 20
DB 96 GSGRGDGLAPRYARQL 114

RESULT 10
Q8V443 PRELIMINARY; PRT; 126 AA.
AC Q8V443
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE VP1 (Fragment).
OS Foot-and-mouth disease virus A.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_Taxid=12111;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KEN/1/76;
RA van Rensburg H.G., Bastos A.D., Haydon D., Joubert F., Nel L.H.;
RT "Gene heterogeneity in the leader and 3C proteinases of foot-and-mouth
disease virus."
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF390861; AAL73359.1; -.
DR InterPro; IPR004080; FMDVp1coat.
DR InterPro; IPR001676; Rhv.
DR Pfam; PF00073; rhv; 1.
DR PRINTS; PR01542; FMDVp1coat.
FT NON_TER 1 1
FT NON_TER 126 126
SQ SEQUENCE 126 AA; 13693 MW; 82675FAC45F713BB CRC64;

Query Match 62.5%; Score 65; DB 12; Length 126;
Best Local Similarity 77.8%; Pred. No. 0.012;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 GSGVGDGSLAPRYARQL 20
DB 54 GSGRGDGLAPRYARQL 71

RESULT 11
Q9YPU0 PRELIMINARY; PRT; 143 AA.
AC Q9YPU0
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE VP1 protein (Fragment).
GN VP1.
```

```
OS Foot-and-mouth disease virus A.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_Taxid=12111;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NM/XZ/64;
RA Liu Z., Zhao Q., Liu W., Xie Q.;
RT "Analysis of VP1 coding nucleotide sequences of six strains of foot-
and-mouth disease virus type A."
RL Ping Tu Hsueh Pao 14:60-67(1998).
DR EMBL; AJ131664; CA10474.1; -.
DR InterPro; IPR004080; FMDVp1coat.
DR InterPro; IPR001676; Rhv.
DR Pfam; PF00073; rhv; 1.
DR PRINTS; PR01542; FMDVp1coat.
FT NON_TER 1 1
FT NON_TER 143 143
SQ SEQUENCE 143 AA; 15881 MW; CF0CC1858CC331E0 CRC64;

Query Match 59.6%; Score 62; DB 12; Length 143;
Best Local Similarity 72.2%; Pred. No. 0.042;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 GSGVGDGSLAPRYARQL 20
DB 71 AGRGDGLAPRYARQL 88

RESULT 12
Q8JUR8 PRELIMINARY; PRT; 208 AA.
AC Q8JUR8
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE ID protein (Fragment).
GN POL.
OS Foot-and-mouth disease virus A.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_Taxid=12111;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/IND/170/88;
RX MEDLINE=21954626; PubMed=11958451;
RA Tosh C., Sanyal A., Hemadri D., Venkataramanan R.;
RT "Phylogenetic analysis of serotype A foot-and-mouth disease virus
isolated in India between 1977 and 2000."
RL Arch. Virol. 147:493-513(2002).
DR EMBL; AF390612; AAM63984.1; -.
DR InterPro; IPR004080; FMDVp1coat.
DR InterPro; IPR001676; Rhv.
DR Pfam; PF00073; rhv; 1.
DR PRINTS; PR01542; FMDVp1coat.
FT NON_TER 1 1
FT NON_TER 208 208
SQ SEQUENCE 208 AA; 22607 MW; 6CE616F86E60CF7E CRC64;

Query Match 59.6%; Score 62; DB 12; Length 208;
Best Local Similarity 68.4%; Pred. No. 0.064;
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 GSGVGDGSLAPRYARQL 20
DB 140 GAGRGDGLAPRYARQL 158

RESULT 13
Q8JUP0 PRELIMINARY; PRT; 211 AA.
AC Q8JUP0
DT 01-OCT-2002 (TREMblrel. 22, Created)
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| QY | DB | Seq | Match | Score | DB | Length | Gaps |
|---|---|---|---|--------|-----|--------|------|
| 01-0Ct-2002 (TREMblrel. 22, Last sequence update) | 01-0Ct-2002 (TREMblrel. 22, Last sequence update) | 01-MAR-2003 (TREMblrel. 23, Last annotation update) | 1D protein (Fragment). | 59.68; | 62; | 211; | 0; |
| GN | GN | GN | Foot-and-mouth disease virus A. | 68.48; | 12; | 211; | 0; |
| OC | OC | OC | Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; | 0.065; | 4; | 211; | 0; |
| OX | OX | OX | NCBI_TaxID=12111; | 0.065; | 4; | 211; | 0; |
| RA | RA | RA | ["Phylogenetic analysis of serotype A foot-and-mouth disease virus isolated in India between 1977 and 2000."; | 0.065; | 4; | 211; | 0; |
| RL | RL | RL | Arch. Virol. 147:493-513(2002). | 0.065; | 4; | 211; | 0; |
| DR | DR | DR | EMBL; AF390641; AAM64012.1; | 0.065; | 4; | 211; | 0; |
| DR | DR | DR | InterPro; IPR004080; FMDVpiccoat. | 0.065; | 4; | 211; | 0; |
| DR | DR | DR | InterPro; IPR001676; RHV. | 0.065; | 4; | 211; | 0; |
| DR | DR | DR | Pfam; PF00073; rhv.1 | 0.065; | 4; | 211; | 0; |
| DR | DR | DR | PRINTS; PR01542; FMDVpiccoat. | 0.065; | 4; | 211; | 0; |
| FT | FT | FT | NON_TER | 0.065; | 4; | 211; | 0; |
| FT | FT | FT | NON_TER | 0.065; | 4; | 211; | 0; |
| SEQ | SEQ | SEQ | SEQUENCE | 0.065; | 4; | 211; | 0; |
| Query Match | Query Match | Query Match | Query Match | 0.065; | 4; | 211; | 0; |
| Best Local Similarity | Best Local Similarity | Best Local Similarity | Best Local Similarity | 0.065; | 4; | 211; | 0; |
| Matches | Matches | Matches | Matches | 0.065; | 4; | 211; | 0; |
| Conservative | Conservative | Conservative | Conservative | 0.065; | 4; | 211; | 0; |
| Mismatches | Mismatches | Mismatches | Mismatches | 0.065; | 4; | 211; | 0; |
| Indels | Indels | Indels | Indels | 0.065; | 4; | 211; | 0; |
| Gaps | Gaps | Gaps | Gaps | 0.065; | 4; | 211; | 0; |

| RESULT 14 | | | |
|-----------|--|--------------|-----------------------------------|
| Q8JUP1 | | | |
| ID | Q8JUP1 | PRELIMINARY; | PRT; 212 AA. |
| AC | Q8JUP1; | | |
| DT | 01-OCT-2002 (TREMblrel. 22, Created) | | |
| DT | 01-OCT-2002 (TREMblrel. 22, Last sequence update) | | |
| DT | 01-MAR-2003 (TREMblrel. 23, Last annotation update) | | |
| DE | 1D protein (Fragment). | | |
| GN | POL. | | |
| OS | Foot-and-mouth disease virus A. | | |
| OC | Viruses; ssRNA positive-strand viruses, no DNA stage: Picornaviridae | | |
| OC | Aphthovirus. | | |
| OX | NCBI_TaxID:12111; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | STRAIN=A/IND/299/99; | | |
| RA | MEDLINE=21954626; PubMed=11958451; | | |
| RA | Tosh C., Saayal A., Hemadri D., Venkataramanan R.; | | |
| RT | "Phylogenetic analysis of serotype A foot-and-mouth disease virus isolated in India between 1977 and 2000."; | | |
| RL | Arch. Virol. 147:493-513(2002). | | |
| DR | EMBL; AF390640; AAM64011.1; - | | |
| DR | InterPro: IPR004080; FMDVp1coat. | | |
| DR | InterPro: IPR001676; Rhv. | | |
| DR | Pfam; PF00073; fhv; 1. | | |
| DR | PRINTS; PR01542; FMDVp1COAT. | | |
| FT | NON_TER | 1 | 1 |
| FT | NON_TER | 212 | 212 |
| SEQ | SEQUENCE | 212 AA; | 23150 MW; E6B690890042CD3A CRC64; |

| | | | | |
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| Query Match | 59.6% | Score 62 | DB 12 | Length 212 |
| Best Local Similarity | 68.4% | Pred. NO. 0.065 | | |
| Matches 13, Conservative | 2 | Mismatches | 4 | Indels 0; Gaps 0; |

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QY      2 GSGVRGDEFGSLAPRVARQL 20
          | : | | | | : | | | | |
Db     139 GTGRKGDLGALARVAQL 157
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| Query Match | Best Local Similarity | Matches | 13: Conservative | 2: Mismatches | 4: Indels | 0: Gaps | | | | | |
|-------------|-----------------------|---------|------------------|---------------|-----------|---------|----|----|----|----|-----|
| 0Y | 2 | GS | GV | RG | DG | SL | AP | RV | AR | OL | 20 |
| DB | 140 | GT | GG | RG | DG | SL | AP | RV | AR | OL | 158 |

Search completed: October 9, 2003, 10:17:34
Job time : 52.3333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 10:11:24 ; Search time 17.3333 Seconds
(without alignments)
48.820 Million cell updates/sec

Title: US-09-549-186b-7

Perfect score: 104

Sequence: 1 CGSGVRCDFGSLAPRVARQL 20

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCrus.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 104 | 100.0 | 20 | 4 | US-08-716-249-7 |
| 2 | 95 | 91.3 | 35 | 3 | US-09-100-600A-1 |
| 3 | 95 | 91.3 | 46 | 3 | US-09-100-600A-38 |
| 4 | 95 | 91.3 | 75 | 3 | US-09-100-600A-28 |
| 5 | 94 | 90.4 | 20 | 4 | US-08-716-249-8 |
| 6 | 92 | 88.5 | 31 | 1 | US-08-418-716A-4 |
| 7 | 91 | 87.5 | 31 | 1 | US-08-418-716A-5 |
| 8 | 91 | 87.5 | 31 | 1 | US-08-418-716A-6 |
| 9 | 89.5 | 86.1 | 19 | 4 | US-08-716-249-2 |
| 10 | 89 | 85.6 | 31 | 1 | US-08-418-716A-2 |
| 11 | 88 | 84.6 | 31 | 1 | US-08-418-716A-1 |
| 12 | 88 | 84.6 | 31 | 1 | US-08-418-716A-7 |
| 13 | 87 | 83.7 | 35 | 3 | US-09-100-600A-2 |
| 14 | 87 | 83.7 | 46 | 3 | US-09-100-600A-3 |
| 15 | 87 | 83.7 | 65 | 3 | US-09-100-600A-27 |
| 16 | 87 | 83.7 | 75 | 3 | US-09-100-600A-29 |
| 17 | 86 | 82.7 | 20 | 4 | US-08-716-249-9 |
| 18 | 76 | 73.1 | 31 | 1 | US-08-418-716A-3 |
| 19 | 71.5 | 68.8 | 19 | 4 | US-08-716-249-1 |
| 20 | 71 | 68.3 | 35 | 3 | US-09-100-600A-8 |
| 21 | 71 | 68.3 | 46 | 3 | US-09-100-600A-42 |
| 22 | 71 | 68.3 | 46 | 3 | US-09-100-600A-49 |
| 23 | 71 | 68.3 | 46 | 3 | US-09-100-600A-50 |
| 24 | 67 | 64.4 | 46 | 3 | US-09-100-600A-43 |
| 25 | 67 | 64.4 | 46 | 3 | US-09-100-600A-44 |
| 26 | 67 | 64.4 | 46 | 3 | US-09-100-600A-48 |
| 27 | 66 | 63.5 | 46 | 3 | US-09-100-600A-45 |

| | | | | | | |
|----|----|------|-----|---|----------------------|--------------------|
| 28 | 63 | 60.6 | 35 | 3 | US-09-100-600A-9 | Sequence 9, Appl |
| 29 | 63 | 60.6 | 55 | 3 | US-09-100-600A-33 | Sequence 33, Appl |
| 30 | 60 | 57.7 | 46 | 3 | US-09-100-600A-39 | Sequence 39, Appl |
| 31 | 59 | 56.7 | 46 | 3 | US-09-100-600A-46 | Sequence 46, Appl |
| 32 | 55 | 52.9 | 45 | 3 | US-09-100-600A-55 | Sequence 55, Appl |
| 33 | 54 | 51.9 | 46 | 3 | US-09-100-600A-47 | Sequence 47, Appl |
| 34 | 53 | 51.0 | 45 | 3 | US-09-100-600A-60 | Sequence 60, Appl |
| 35 | 50 | 48.1 | 45 | 3 | US-09-100-600A-61 | Sequence 51, Appl |
| 36 | 50 | 48.1 | 45 | 3 | US-09-100-600A-62 | Sequence 62, Appl |
| 37 | 50 | 48.1 | 45 | 3 | US-09-100-600A-64 | Sequence 64, Appl |
| 38 | 50 | 48.1 | 45 | 3 | US-09-100-600A-65 | Sequence 65, Appl |
| 39 | 50 | 48.1 | 46 | 3 | US-09-100-600A-41 | Sequence 40, Appl |
| 40 | 50 | 48.1 | 46 | 3 | US-09-100-600A-41 | Sequence 41, Appl |
| 41 | 49 | 47.1 | 387 | 4 | US-09-252-991A-17881 | Sequence 17881, A |
| 42 | 48 | 46.2 | 45 | 3 | US-09-100-600A-56 | Sequence 56, Appl |
| 43 | 48 | 46.2 | 387 | 4 | US-09-252-991A-18477 | Sequence 18477, A |
| 44 | 46 | 44.2 | 20 | 6 | US-04096-32 | Patent No. 5204096 |
| 45 | 46 | 44.2 | 45 | 3 | US-09-100-600A-52 | Sequence 52, Appl |

ALIGNMENTS

RESULT 1
US-08-716-249-7
Sequence 7, Application US/08716249
Patent No. 6455244
GENERAL INFORMATION:
APPLICANT: Guichard, Gilles
APPLICANT: Muller, Sylviane
APPLICANT: Briand, Jean-Paul
APPLICANT: Regemortel, Marc
TITLE OF INVENTION: Retropeptides, Antibodies Thereof, and
TITLE OF INVENTION: Uses Thereof for Vaccination and In Vitro Diagnosis
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spencer & Frank
STREET: 1100 New York Avenue, Suite 300E
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,249
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/00292
FILING DATE: 13-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Calvetti, Frederick F.
REGISTRATION NUMBER: 28,557
REFERENCE/DOCKET NUMBER: GROFO 7001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)414-4000
TELEFAX: (202)414-4040
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-716-249-7
Query Match 100.0%; Score 104; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 CGSGVRGDEGSLAPVARÖL 20
        |||||
Db      1 CGSGVRGDEGSLAPVARÖL 20
```

RESULT 2
ITS-09-10

```

US-09-100-600A-1
: Sequence 1, Application US/09100600A
: Patent No. 6107021
:
: GENERAL INFORMATION:
:
:   APPLICANT: Wang, Chang Yi
:   APPLICANT: Shen, Ming
:   TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR
:   TITLE OF INVENTION: FOOT-AND-MOUTH DISEASE
:   NUMBER OF SEQUENCES: 91
:
:   CORRESPONDENCE ADDRESSES:
:     ADDRESSEE: Morgan & Finnegan, L.L.P.
:     STREET: 345 Park Avenue
:     CITY: New York
:     STATE: NY
:
:   COUNTRY: USA
:   ZIP: 10154-0054
:
:   COMPUTER READABLE FORM:
:     MEDIUM TYPE: Floppy disk
:     COMPUTER: IBM PC compatible
:     OPERATING SYSTEM: Windows 95
:     SOFTWARE: Word 97
:
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/09/100,600A
:     FILING DATE: 20-Jun-1998
:     CLASSIFICATION: 42A
:
:   ATTORNEY/AGENT INFORMATION:
:     NAME: Maria C.H. Lin
:     REGISTRATION NUMBER: 29,323
:     REFERENCE/DOCKET NUMBER: 1151-4156
:
:   TELECOMMUNICATION INFORMATION:
:     TELEPHONE: 212-758-4800
:     TELEFAX: 212-751-6849
:
:   INFORMATION FOR SEQ ID NO: 1:
:     SEQUENCE CHARACTERISTICS:
:       LENGTH: 35 amino acids
:       TYPE: amino acid
:       TOPOLOGY: linear
:
:   MOLECULE TYPE: peptide
:
: US-09-100-600A-1

```

| | | | | |
|--------------------------|--------|------------|---------|------------------|
| Query Match | 91.3% | Score 95 | DB 3 | Length 35 |
| Best Local Similarity | 100.0% | Pred. NO. | 4.3e-08 | |
| Matches 19; Conservative | 0; | Mismatches | 0; | Indels 0; Gaps 0 |

RESULT 3
HS-09-100-600A-38

Sequence 38, Application US/09100600A
Patent No. 6107021
GENERAL INFORMATION:
APPLICANT: Wang, Chang YI
APPLICANT: Shen, Ming
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR
TITLE OF INVENTION: FOOT-AND-MOUTH DISEASE
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; COMMAND: Head 07

```

| | | | | |
|--------------------------|--------|------------|----------|-------------------|
| Query Match | 91.3% | Score 95: | DB 3: | Length 46: |
| Best Local Similarity | 100.0% | Pred. No. | 5.8e-08: | |
| Matches 19; Conservative | 0; | Mismatches | 0; | Indels 0; Gaps 0; |

RESULT 4

Sequence 28, Application US/09100600A
Patent No. 6107021
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
APPLICANT: Shen, Ming
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR
FOOT-AND-MOUTH DISEASE
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,600A
FILING DATE: 20-Jun-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,322
REFERENCE/DOCKET NUMBER: 1151-4156
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEO ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-600A-28

Query Match 91.3%; Score 95; DB 3; Length 75;
Best Local Similarity 100.0%; Pred. No. 9.6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSGVGRDGFSLAPRVAROL 20
DB 47 GSGVGRDGFSLAPRVAROL 65

RESULT 5

US-08-716-249-8
; Sequence 8, Application US/08716249
; Patent No. 6455244
; GENERAL INFORMATION:
; APPLICANT: Gulchard, Gilles
; APPLICANT: Muller, Sylviane
; APPLICANT: Briand, Jean-Paul
; APPLICANT: Regemortel, Marc
; TITLE OF INVENTION: Retropeptides, Antibodies thereo, and
; TITLE OF INVENTION: Uses thereof for Vaccination and In Vitro Diagnosis
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spencer & Frank
; STREET: 1100 New York Avenue, Suite 300E
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,249
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/00292
; FILING DATE: 13-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Calvetti, Frederick F.
; REGISTRATION NUMBER: 28,557
; REFERENCE/DOCKET NUMBER: GROFO 7001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)414-4000
; TELEFAX: (202)414-4040
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
US-08-716-249-8

Query Match 90.4%; Score 94; DB 4; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.4e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSGVGRDGFSLAPRVAROL 20
DB 1 GSGVGRDGFSLAPRVAROL 20

RESULT 6

US-08-418-716A-4
; Sequence 4, Application US/08418716A
; Patent No. 5612040
; GENERAL INFORMATION:
; APPLICANT: Mason, Peter W.
; APPLICANT: Baxt, Barry

APPLICANT: Reider, Elizabeth
APPLICANT: Berinstein, Analia
APPLICANT: Kang, Angray S
TITLE OF INVENTION: No. 5612040-Infectious Foot-and-Mouth Disease
TITLE OF INVENTION: Viruses
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESSEE: Janelle S. Graeter
STREET: Rm. 411, Bldg. 005, BARC-W
CITY: Beltsville
STATE: Maryland
COUNTRY: USA
ZIP: 20705

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,716A
FILING DATE:
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Graeter, Janelle S.
REGISTRATION NUMBER: 35,024
REFERENCE/DOCKET NUMBER: 0137.94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 504-6629
TELEFAX: (301) 504-5060
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Foot and mouth disease virus

US-08-418-716A-4

Query Match 88.5%; Score 92; DB 1; Length 31;
Best Local Similarity 94.7%; Pred. No. 1.1e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSGVGRDGFSLAPRVAROL 20
DB 11 GSGVGRDGFSLAPRVAROL 29

RESULT 7

US-08-418-716A-5
; Sequence 5, Application US/08418716A
; Patent No. 5612040
; GENERAL INFORMATION:
; APPLICANT: Mason, Peter W.
; APPLICANT: Baxt, Barry
; APPLICANT: Reider, Elizabeth
; APPLICANT: Berinstein, Analia
; APPLICANT: Kang, Angray S
; TITLE OF INVENTION: No. 5612040-Infectious Foot-and-Mouth Disease
; TITLE OF INVENTION: Viruses
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janelle S. Graeter
; STREET: Rm. 411, Bldg. 005, BARC-W
; CITY: Beltsville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20705
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,716A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Graeter, Janelle S.
REGISTRATION NUMBER: 35,024
REFERENCE/DOCKET NUMBER: 0137.94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 504-5060
TELEFAX: (301) 504-5060
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Foot and mouth disease virus
US-08-418-716A-5

Query Match 87.5%; Score 91; DB 1; Length 31;
Best Local Similarity 94.7%; Pred. No. 1.6e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSGVRGDFGSLAPVAROL 20
DB 11 GSGVRGDFGSLAPVAROL 29

RESULT 8
US-08-418-716A-6
Sequence 6, Application US/08418716A
Patent No. 5612040
GENERAL INFORMATION:
APPLICANT: Mason, Peter W.
APPLICANT: Baxt, Barry
APPLICANT: Reider, Elizabeth
APPLICANT: Bernstein, Analia
APPLICANT: Kang, Angray S
TITLE OF INVENTION: No. 5612040-Infectious Foot-and-Mouth Disease
TITLE OF INVENTION: Viruses
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janelle S. Graeter
STREET: Rm. 411, Bldg. 005, BARC-W
CITY: Beltsville
STATE: Maryland
COUNTRY: USA
ZIP: 20705
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,716A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Graeter, Janelle S.
REGISTRATION NUMBER: 35,024
REFERENCE/DOCKET NUMBER: 0137.94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 504-6629
TELEFAX: (301) 504-5060
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Foot and mouth disease virus
US-08-418-716A-6

Query Match 87.5%; Score 91; DB 1; Length 31;
Best Local Similarity 94.7%; Pred. No. 1.6e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSGVRGDFGSLAPVAROL 20
DB 11 GSGVRGDFGSLAPVAROL 29

RESULT 9
US-08-716-249-2
Sequence 2, Application US/08716249
Patent No. 6455244
GENERAL INFORMATION:
APPLICANT: Guichard, Gilles
APPLICANT: Muller, Sylviane
APPLICANT: Briand, Jean-Paul
APPLICANT: Regemortel, Marc
TITLE OF INVENTION: Retropeptides, Antibodies Thereof, and
TITLE OF INVENTION: Uses Thereof for Vaccination and In Vitro Diagnosis
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spencer & Frank
STREET: 1100 New York Avenue, Suite 300E
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,249
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/00292
FILING DATE: 13-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Calvetil, Frederick F.
REGISTRATION NUMBER: 28,557
REFERENCE/DOCKET NUMBER: GROFO 7001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)414-4000
TELEFAX: (202)414-4040
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-716-249-2

Query Match 86.1%; Score 89.5; DB 4; Length 19;
Best Local Similarity 95.0%; Pred. No. 1.6e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CGSGVRGDFGSLAPVAROL 20

Db 1 CGSGVGDGFGSLAPVAROL 19

RESULT 10
US-08-418-716A-2
; Sequence 2, Application US/08418716A
; Patent No. 5612040
; GENERAL INFORMATION:
; APPLICANT: Mason, Peter W.
; APPLICANT: Baxt, Barry
; APPLICANT: Reider, Elizabeth
; APPLICANT: Bernstein, Analia
; APPLICANT: Kang, Angray S
; TITLE OF INVENTION: No. 5612040-Infectious Foot-and-Mouth Disease
; TITLE OF INVENTION: Viruses
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janelle S. Graeter
; STREET: Rm. 411, Bldg. 005, BARC-W
; CITY: Beltsville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20705
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/418,716A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Graeter, Janelle S.
; REGISTRATION NUMBER: 35,024
; REFERENCE/DOCKET NUMBER: 0137.94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 504-5629
; TELEFAX: (301) 504-5060
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE:
; ORGANISM: Foot and mouth disease virus
; US-08-418-716A-2

Query Match 85.6%; Score 89; DB 1; Length 31;
Best Local Similarity 94.7%; Pred. No. 3.2e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGVGDGFGSLAPVAROL 20
Db 11 GSGRGDGFGSLAPVAROL 29

RESULT 11
US-08-418-716A-1
; Sequence 1, Application US/08418716A
; Patent No. 5612040
; GENERAL INFORMATION:
; APPLICANT: Mason, Peter W.
; APPLICANT: Baxt, Barry
; APPLICANT: Reider, Elizabeth
; APPLICANT: Bernstein, Analia
; APPLICANT: Kang, Angray S
; TITLE OF INVENTION: No. 5612040-Infectious Foot-and-Mouth Disease

;; TITLE OF INVENTION: Viruses
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Janelle S. Graeter
;; STREET: Rm. 411, Bldg. 005, BARC-W
;; CITY: Beltsville
;; STATE: Maryland
;; COUNTRY: USA
;; ZIP: 20705
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/418,716A
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Graeter, Janelle S.
;; REGISTRATION NUMBER: 35,024
;; REFERENCE/DOCKET NUMBER: 0137.94
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (301) 504-5629
;; TELEFAX: (301) 504-5060
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 31 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; FRAGMENT TYPE: Internal
;; ORIGINAL SOURCE:
;; ORGANISM: Foot and mouth disease virus
; US-08-418-716A-1

Query Match 84.6%; Score 88; DB 1; Length 31;
Best Local Similarity 94.7%; Pred. No. 4.6e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGVGDGFGSLAPVAROL 20
Db 11 GSGRGDGFGSLAPVAROL 29

RESULT 12
US-08-418-716A-7
; Sequence 7, Application US/08418716A
; Patent No. 5612040
; GENERAL INFORMATION:
; APPLICANT: Mason, Peter W.
; APPLICANT: Baxt, Barry
; APPLICANT: Reider, Elizabeth
; APPLICANT: Bernstein, Analia
; APPLICANT: Kang, Angray S
; TITLE OF INVENTION: No. 5612040-Infectious Foot-and-Mouth Disease
; TITLE OF INVENTION: Viruses
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janelle S. Graeter
; STREET: Rm. 411, Bldg. 005, BARC-W
; CITY: Beltsville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20705
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/418,716A
FILING DATE: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Graeter, Janelle S.
REGISTRATION NUMBER: 35,024
REFERENCE/DOCKET NUMBER: 0137.94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 504-6629
TELEFAX: (301) 504-5060
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEetical: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE: Internal
US-08-418-716A-7

Query Match 84.6%; Score 88; DB 1; Length 31;
Best Local Similarity 89.5%; Pred. No. 4.6e-07;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 GSGVRGDFGSLAPVARQL 20
Db 11 GSGVRGDFGSLAPVARQL 29

RESULT 13
US-09-100-600A-2
Sequence 2, Application US/09100600A
Patent No. 6107021
GENERAL INFORMATION:
APPLICANT: Wang, Chang Y1
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR
FOOT-AND-MOUTH DISEASE
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,600A
FILING DATE: 20-Jun-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4156
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-600A-2

Query Match 83.7%; Score 87; DB 3; Length 35;
Best Local Similarity 94.7%; Pred. No. 7.4e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GSGVRGDFGSLAPVARQL 20
Db 7 GSGVRGDFGSLAPVARCL 25

RESULT 14
US-09-100-600A-3
Sequence 3, Application US/09100600A
Patent No. 6107021
GENERAL INFORMATION:
APPLICANT: Wang, Chang Y1
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR
FOOT-AND-MOUTH DISEASE
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,600A
FILING DATE: 20-Jun-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4156
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-600A-3

Query Match 83.7%; Score 87; DB 3; Length 46;
Best Local Similarity 94.7%; Pred. No. 9.9e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GSGVRGDFGSLAPVARQL 20
Db 16 GSGVRGDFGSLAPVARCL 34

RESULT 15
US-09-100-600A-27
Sequence 27, Application US/09100600A
Patent No. 6107021
GENERAL INFORMATION:
APPLICANT: Wang, Chang Y1
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR
FOOT-AND-MOUTH DISEASE
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York

STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,600A
FILING DATE: 20-Jun-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4156
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 65 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-600A-27

Query Match 83.7%; Score 87; DB 3; Length 65;
Best Local Similarity 94.7%; Pred. No. 1.4e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GSGVGRDGSILAPRVARQL 20
|||||
Db 47 GSGVGRDGSILAPRVARCL 65

Search completed: October 9, 2003, 10:19:37
Job time : 17.3333 secs

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OM protein - protein search, using sw model

Run on: October 9, 2003, 10:14:31 ; Search time 21.3333 Seconds

(without alignments)
151,058 Million cell updates/sec

Title: US-09-549-186b-7

Perfect score: 104

Sequence: 1 CGSGVRGDFGSLAPRAVRL 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PTI_NEW_PUB.pep:*
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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 44 | 42.3 | 920 | 15 | US-10-156-761-14172 |
| 2 | 44 | 42.3 | 920 | 15 | US-09-983-531A-4 |
| 3 | 44 | 42.3 | 998 | 15 | US-10-101-464A-931 |
| 4 | 43 | 41.3 | 312 | 15 | US-10-207-655-186 |
| 5 | 43 | 41.3 | 476 | 9 | US-09-291-299A-3 |
| 6 | 43 | 41.3 | 627 | 15 | US-10-222-100-3 |
| 7 | 43 | 41.3 | 974 | 15 | US-10-101-464A-921 |
| 8 | 42 | 40.4 | 184 | 15 | US-10-156-761-14999 |
| 9 | 42 | 40.4 | 232 | 15 | US-10-101-464A-515 |
| 10 | 42 | 40.4 | 630 | 15 | US-10-195-117-2 |
| 11 | 42 | 40.4 | 960 | 8 | US-08-910-386A-18 |
| 12 | 42 | 40.4 | 1021 | 15 | US-10-101-464A-954 |
| 13 | 41.5 | 39.9 | 446 | 10 | US-09-738-626-6262 |
| 14 | 41 | 38.4 | 261 | 10 | US-10-156-761-9294 |
| 15 | 41 | 39.4 | 653 | 11 | US-09-820-843A-26 |

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| 16 | 41 | 39.4 | 4123 | 15 | US-10-213-509-5 | Sequence 5, Appl1 |
| 17 | 40 | 38.5 | 28 | 9 | US-09-864-761-34511 | Sequence 34511, A |
| 18 | 40 | 38.5 | 94 | 15 | US-10-102-806-581 | Sequence 581, App |
| 19 | 40 | 38.5 | 124 | 16 | US-10-080-170-376 | Sequence 376, App |
| 20 | 40 | 38.5 | 142 | 9 | US-09-908-711-105 | Sequence 105, App |
| 21 | 40 | 38.5 | 142 | 11 | US-09-764-891-3245 | Sequence 3245, App |
| 22 | 40 | 38.5 | 173 | 15 | US-10-156-761-12492 | Sequence 12492, A |
| 23 | 40 | 38.5 | 199 | 10 | US-09-921-640-6 | Sequence 6, Appl1 |
| 24 | 40 | 38.5 | 258 | 15 | US-09-921-640-9 | Sequence 9, Appl1 |
| 25 | 40 | 38.5 | 294 | 15 | US-10-102-806-595 | Sequence 595, App |
| 26 | 40 | 38.5 | 394 | 15 | US-10-156-761-8790 | Sequence 8790, App |
| 27 | 40 | 38.5 | 437 | 15 | US-10-156-761-10200 | Sequence 10200, A |
| 28 | 40 | 38.5 | 907 | 14 | US-10-008-739A-2 | Sequence 2, Appl1 |
| 29 | 40 | 38.5 | 1014 | 9 | US-09-912-020-266 | Sequence 266, App |
| 30 | 40 | 38.5 | 1150 | 10 | US-09-870-122-3 | Sequence 3, Appl1 |
| 31 | 40 | 38.5 | 1161 | 8 | US-08-910-386A-20 | Sequence 20, Appl1 |
| 32 | 40 | 38.5 | 1164 | 10 | US-09-870-122-1 | Sequence 1, Appl1 |
| 33 | 40 | 38.5 | 1167 | 10 | US-09-870-122-2 | Sequence 2, Appl1 |
| 34 | 40 | 38.5 | 1181 | 10 | US-09-870-122-3 | Sequence 3, Appl1 |
| 35 | 39.5 | 38.0 | 195 | 15 | US-10-156-761-7790 | Sequence 7790, App |
| 36 | 39 | 37.5 | 19 | 11 | US-09-931-325A-145 | Sequence 145, App |
| 37 | 39 | 37.5 | 19 | 12 | US-09-931-325A-146 | Sequence 146, App |
| 38 | 39 | 37.5 | 26 | 11 | US-09-931-325A-145 | Sequence 145, App |
| 39 | 39 | 37.5 | 26 | 12 | US-09-930-915A-187 | Sequence 187, App |
| 40 | 39 | 37.5 | 31 | 12 | US-09-930-915A-7 | Sequence 7, Appl1 |
| 41 | 39 | 37.5 | 31 | 12 | US-10-082-014-13 | Sequence 13, Appl1 |
| 42 | 39 | 37.5 | 118 | 9 | US-09-864-761-33856 | Sequence 33856, A |
| 43 | 39 | 37.5 | 199 | 15 | US-10-152-300-2 | Sequence 2, Appl1 |
| 44 | 39 | 37.5 | 211 | 10 | US-09-738-626-5094 | Sequence 5094, App |
| 45 | 39 | 37.5 | 216 | 9 | US-09-908-180-4 | Sequence 4, Appl1 |

ALIGNMENTS

RESULT 1
US-10-156-761-14172
; Sequence 14172, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 14172
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
; US-10-156-761-14172

Query Match 42.3%; Score 44; DB 15; Length 240;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GVRGDFGSLAPR 15
| ||| |||||
DB 212 GDTGDFASLAPR 223

RESULT 2
US-09-983-531A-4

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; Sequence 4, Application US/09983531A
; Patent No. US20020147132A1
; GENERAL INFORMATION:
; APPLICANT: Fujisawa, Atsuko
; APPLICANT: Yamakawa, Toru
; APPLICANT: Shitakawa, Kamon
; APPLICANT: Chitose, Oriti
; APPLICANT: Ogawa, Naoki
; TITLE OF INVENTION: Meltrins
; FILE REFERENCE: 11-22-99 sequence submission
; CURRENT APPLICATION NUMBER: US/09/983,531A
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: JP 8-61756
; PRIOR FILING DATE: 1996-02-23
; PRIOR APPLICATION NUMBER: PCT/JP96/03017
; PRIOR FILING DATE: 1996-10-17
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 920
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Clone:
; OTHER INFORMATION: JM109(pBSMcl-beta), mouse beta meltrin
; NAME/KEY: Unsure
; LOCATION: 574
; OTHER INFORMATION: Amino acid "Xaa" is unknown
US-09-983-531A-4

Query Match          42.3%; Score 44; DB 10; Length 920;
Best Local Similarity 38.9%; Pred. No. 1.8e+02;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY      1 CGSGRGDFGSLAPVAR 18
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Db      555 CGKGLNGQYRKCSPRDAK 572

RESULT 3
US-10-101-464A-931
; Sequence 931, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 931
; LENGTH: 998
; TYPE: PRT
; ORGANISM: Pinus radiata
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(998)
; OTHER INFORMATION: Xaa - Any Amino Acid
US-10-101-464A-931

Query Match          42.3%; Score 44; DB 15; Length 998;
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Best Local Similarity 38.5%; Pred. No. 2e+02;
Matches 10; Conservative 3; Mismatches 7; Indels 6; Gaps 1;

QY      1 CGSG-----VRCDFGSLAPVARQL 20
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Db      849 CGSGADSMFALAGSYGIAPREYATTL 874

RESULT 4
US-10-207-655-186
; Sequence 186, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 186
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-186

Query Match          41.3%; Score 43; DB 15; Length 312;
Best Local Similarity 61.5%; Pred. No. 84;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 CGSGRGDFGSLA 13
      |||| | | | | |
Db      164 CGSGARGGDEVA 176

RESULT 5
US-09-291-299A-3
; Sequence 3, Application US/09291299A
; Patent No. US20020076405A1
; GENERAL INFORMATION:
; APPLICANT: Yong, Xie
; TITLE OF INVENTION: Antigenized Antibody Vaccine for Foot-and-Mouth Disease
; FILE REFERENCE: 09/291,299
; CURRENT APPLICATION NUMBER: US/09/291,299A
; CURRENT FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Sus sp.
US-09-291-299A-3

Query Match          41.3%; Score 43; DB 9; Length 476;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 11; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY      1 CGS--GVRGDFGSLAPVARQL 20
      || | | | | | | | | | |
Db      115 CGKVPNLRGDLQYLAQKVARTL 136

RESULT 6
US-10-222-100-3
; Sequence 3, Application US/10222100
; Publication No. US20030059439A1
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut Voor Biotechnologie VZW
; APPLICANT: Revets, Hilde
; APPLICANT: Cornelis, Pierre
; APPLICANT: De Baetselier, Patrick
; TITLE OF INVENTION: THI INDUCING NATURAL ADJUVANT FOR HETEROLOGOUS ANTIGENS
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;; FILE REFERENCE: 2676-5449US
;; CURRENT APPLICATION NUMBER: US/10/222.100
;; CURRENT FILING DATE: 2002-08-16
;; PRIOR APPLICATION NUMBER: PCT/EP01/01673
;; PRIOR FILING DATE: 2000-02-18
;; NUMBER OF SEQ ID NOS: 6
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 3
;; LENGTH: 627
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: OPT-3D-FMDV15 fusion
US-10-222-100-3

Query Match
Best Local Similarity 41.3%; Score 43; DB 15; Length 627;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 3 SGVRGDFGSLAPRVAROL 20
   | | | | | | | | | |
Db 573 SNLRGDLQVLAKVARTL 590

RESULT 7
US-10-101-464A-921
;; Sequence 921, Application US/10101464A
;; Publication No. US20030046728A1
;; GENERAL INFORMATION:
;; APPLICANT: Strabala, Timothy
;; APPLICANT: Nieuwenhuizen, Nicolaas
;; TITLE OF INVENTION: Compositions Isolated from Plant Cells
;; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
;; FILE REFERENCE: 11000.1020c2
;; CURRENT APPLICATION NUMBER: US/10/101.464A
;; CURRENT FILING DATE: 2002-03-18
;; PRIOR APPLICATION NUMBER: 09/7704,302
;; PRIOR FILING DATE: 2000-11-01
;; PRIOR APPLICATION NUMBER: 09/228,986
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/162,866
;; PRIOR FILING DATE: 1999-11-01
;; PRIOR APPLICATION NUMBER: PCT/US00/00724
;; PRIOR FILING DATE: 2000-01-11
;; NUMBER OF SEQ ID NOS: 989
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 921
;; LENGTH: 974
;; TYPE: PRT
;; ORGANISM: Eucalyptus grandis
US-10-101-464A-921

Query Match
Best Local Similarity 41.3%; Score 43; DB 15; Length 974;
Matches 9; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 CGSGVRGDFGSLAPRVAROL 20
   | | | | | | | | | |
Db 835 CMSVAGSYGYIAPEYATYL 854

RESULT 8
US-10-156-761-14999
;; Sequence 14999, Application US/10156761
;; Publication No. US20030119018A1
;; GENERAL INFORMATION:
;; APPLICANT: OMURA, SATOSHI
;; APPLICANT: IKEDA, HARUO
;; APPLICANT: ISHIKAWA, JUN
;; APPLICANT: HORIKAWA, HIROSHI
;; APPLICANT: SHIBA, TADAYOSHI
;; APPLICANT: SAKAKI, YOSHITUKI
```

```
;; APPLICANT: HATTORI, MASAHIRA
;; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;; FILE REFERENCE: 249-262
;; CURRENT APPLICATION NUMBER: US/10/156.761
;; CURRENT FILING DATE: 2002-05-29
;; PRIOR APPLICATION NUMBER: JP 2001-204089
;; PRIOR FILING DATE: 2001-05-30
;; PRIOR APPLICATION NUMBER: JP 2001-272697
;; PRIOR FILING DATE: 2001-08-02
;; NUMBER OF SEQ ID NOS: 15109
;; SEQ ID NO 14999
;; LENGTH: 184
;; TYPE: PRT
;; ORGANISM: Streptomyces avermitilis
US-10-156-761-14999

Query Match
Best Local Similarity 40.4%; Score 42; DB 15; Length 184;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 7 GDFGSLAPRVAROL 20
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Db 108 GELGAVSPVAAQV 121

RESULT 9
US-10-101-464A-515
;; Sequence 515, Application US/10101464A
;; Publication No. US20030046728A1
;; GENERAL INFORMATION:
;; APPLICANT: Strabala, Timothy
;; APPLICANT: Nieuwenhuizen, Nicolaas
;; TITLE OF INVENTION: Compositions Isolated from Plant Cells
;; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
;; FILE REFERENCE: 11000.1020c2
;; CURRENT APPLICATION NUMBER: US/10/101.464A
;; CURRENT FILING DATE: 2002-03-18
;; PRIOR APPLICATION NUMBER: 09/7704,302
;; PRIOR FILING DATE: 2000-11-01
;; PRIOR APPLICATION NUMBER: 09/228,986
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/162,866
;; PRIOR FILING DATE: 1999-11-01
;; PRIOR APPLICATION NUMBER: PCT/US00/00724
;; PRIOR FILING DATE: 2000-01-11
;; NUMBER OF SEQ ID NOS: 989
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 515
;; LENGTH: 232
;; TYPE: PRT
;; ORGANISM: Eucalyptus grandis
US-10-101-464A-515

Query Match
Best Local Similarity 40.4%; Score 42; DB 15; Length 232;
Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CGSGVRGDFGSLAPRVAROL 20
   | | | | | | | | | |
Db 204 CMSATAGSYGYIAPEYATYL 223

RESULT 10
US-10-195-117-2
;; Sequence 2, Application US/10195117
;; Publication No. US20030092083A1
;; GENERAL INFORMATION:
;; APPLICANT: In2Gen Co., Ltd.
;; APPLICANT: Jeoung, Doo-Il
;; APPLICANT: Cho, Bomsoo
;; APPLICANT: Lim, Yoon
;; APPLICANT: Park, Saeyoung
```

APPLICANT: Lee, Daeyeon
APPLICANT: Bang, Yung-Jue
APPLICANT: Yang, Hankwang
APPLICANT: Kim, Dae-kee
TITLE OF INVENTION: CAGE Antigen
FILE REFERENCE: 59258-00002
CURRENT APPLICATION NUMBER: US/10/195.117
CURRENT FILING DATE: 2002-07-11
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 630
TYPE: PRT
ORGANISM: Homo sapiens
US-10-195-117-2

Query Match 40.4%; Score 42; DB 15; Length 630;
Best Local Similarity 56.2%; Pred. No. 2.5e+02;
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 GSGVRGDFGSLAPRVA 17
||| | | | | | | |
Db 29 GSGVSGPFGHCGPRAA 44

RESULT 11
US-08-910-386A-18
Sequence 18, Application US/08910386A
Publication No. US20020092041A1
GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C.
APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Hulbert, Scot
APPLICANT: Richter, Todd
TITLE OF INVENTION: Procedures and Materials for Confering
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,386A
FILING DATE: 13-AUG-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Baetian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-058950US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-910-386A-18

Query Match 40.4%; Score 42; DB 8; Length 960;
Best Local Similarity 40.0%; Pred. No. 3.9e+02;
Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CGSGVRGDFGSLAPRVAROL 20
| | : | : | | | | |
Db 835 CMSAIAAGSYGYIAPEVAYTL 854

RESULT 12
US-10-101-464A-954
Sequence 954, Application US/10101464A
Publication No. US20030046728A1
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020C2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 954
LENGTH: 1021
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-10-101-464A-954

Query Match 40.4%; Score 42; DB 15; Length 1021;
Best Local Similarity 40.0%; Pred. No. 4.2e+02;
Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 1 CGSGVRGDFGSLAPRVAROL 20
| | : | : | | | | |
Db 861 CMSAIAAGSYGYIAPEVAYTL 880

RESULT 13
US-09-738-626-6262
Sequence 6262, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: MAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIRO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, MAKOTO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 6262
LENGTH: 446
TYPE: PRT

; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6262

Query Match 39.9%; Score 41.5; DB 10; Length 446;
Best Local Similarity 55.0%; Pred. No. 2.1e+02;
Matches 11; Conservative 2; Mismatches 4; Indels 3; Gaps 1;

OY 4 GVR---GDFGSLAPRVARQL 20
||| ||| ||| :||
Db 261 GVRIDSGDLGVLRKVRKQL 280

RESULT 14
US-10-156-761-9294

; Sequence 9294, Application US/10156761
; Publication No. US20030119018A1

; GENERAL INFORMATION:

; APPLICANT: OMURA, SATOSHI

; APPLICANT: IKEDA, HARUO

; APPLICANT: ISHIKAWA, JUN

; APPLICANT: HORIKAWA, HIROSHI

; APPLICANT: SHIBA, TADAYOSHI

; APPLICANT: SAKAKI, YOSHIYUKI

; APPLICANT: HATTORI, MASAHIRA

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

; FILE REFERENCE: 249-262

; CURRENT APPLICATION NUMBER: US/10/156,761

; CURRENT FILING DATE: 2002-05-29

; PRIOR APPLICATION NUMBER: JP 2001-204089

; PRIOR FILING DATE: 2001-05-30

; PRIOR APPLICATION NUMBER: JP 2001-272697

; PRIOR FILING DATE: 2001-08-02

; NUMBER OF SEQ ID NOS: 15109

; SEQ ID NO 9294

; LENGTH: 261

; TYPE: PRT

; ORGANISM: Streptomyces avermitilis

US-10-156-761-9294

Query Match 39.4%; Score 41; DB 15; Length 261;
Best Local Similarity 52.6%; Pred. No. 1.4e+02;
Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 2 GSGVGDGSLAPRVARQL 20
| | | | | :|||
Db 97 GGSVLDLIGTAYRLARQL 115

RESULT 15
US-09-820-843A-26

; Sequence 26, Application US/09820843A

; Publication No. US20030039963A1

; GENERAL INFORMATION:

; APPLICANT: Council of Scientific and Industrial Research

; TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEIN

; FILE REFERENCE: 063915

; CURRENT APPLICATION NUMBER: US/09/820,843A

; CURRENT FILING DATE: 2001-03-30

; NUMBER OF SEQ ID NOS: 118

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 26

; LENGTH: 653

; TYPE: PRT

; ORGANISM: Vibrio cholerae

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Iron(III) ABC transporter, permease protein

; NAME/KEY: misc_feature

; OTHER INFORMATION: g1|9654609

US-09-820-843A-26

Query Match 39.4%; Score 41; DB 11; Length 653;

Best Local Similarity 52.9%; Pred. No. 3.8e+02;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 4 GVRDGFSLAPRVARQL 20
||| ||| ||| :|||
Db 249 GVIGFGLTPNIRSL 265

Search completed: October 9, 2003, 10:20:48
Job time : 22.333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 10:02:18 ; Search time 58.3333 Seconds

(without alignments)
54.421 Million cell updates/sec

Title: US-09-549-186b-8

Perfect score: 101

Sequence: 1 CGSGVGRDPSGLARVARQL 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*
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24: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match length | ID | Description |
|------------|-------|--------------------|----------------|--------------------|
| 1 | 92 | 91.1 | 19 24 ABU08643 | Foot and mouth dis |
| 2 | 85 | 84.2 | 19 24 ABU08642 | Foot and mouth dis |
| 3 | 85 | 84.2 | 20 21 AAP94587 | Envelope gene epit |
| 4 | 85 | 84.2 | 31 4 AAP30107 | Sequence of VPI ca |
| 5 | 85 | 84.2 | 31 6 AAP50728 | Foot-and-mouth dis |
| 6 | 85 | 84.2 | 31 18 AAM17082 | Foot and mouth dis |
| 7 | 85 | 84.2 | 35 21 AAY68501 | Target antigenic p |
| 8 | 85 | 84.2 | 75 21 AAY68528 | Synthetic foot and |
| 9 | 85 | 84.2 | 216 4 AAP30205 | Sequence encoded b |

| | | | | |
|----|----|------|-----------------|--------------------|
| 10 | 85 | 84.2 | 220 4 AAP30195 | Sequence encoded b |
| 11 | 85 | 84.2 | 233 4 AAP30204 | Sequence encoded b |
| 12 | 85 | 84.2 | 405 4 AAP30202 | Sequence encoded b |
| 13 | 85 | 84.2 | 406 4 AAP30203 | Sequence encoded b |
| 14 | 85 | 84.2 | 609 4 AAP30206 | Sequence encoded b |
| 15 | 84 | 83.2 | 20 14 AAR38543 | Foot and Mouth Dis |
| 16 | 84 | 83.2 | 20 14 AAR41793 | Foot and Mouth Dis |
| 17 | 83 | 82.2 | 31 18 AAM17085 | Foot and Mouth Dis |
| 18 | 82 | 81.2 | 31 18 AAM17086 | Foot and Mouth Dis |
| 19 | 81 | 80.2 | 31 18 AAM17087 | Foot and Mouth Dis |
| 20 | 79 | 78.2 | 31 18 AAM17084 | Foot and Mouth Dis |
| 21 | 78 | 77.2 | 31 18 AAM17083 | Foot and Mouth Dis |
| 22 | 78 | 77.2 | 31 18 AAM17088 | Foot and Mouth Dis |
| 23 | 77 | 76.2 | 35 21 AAY68502 | Target antigenic p |
| 24 | 77 | 76.2 | 46 21 AAY68503 | Target antigenic p |
| 25 | 77 | 76.2 | 65 21 AAY68527 | Synthetic foot and |
| 26 | 77 | 76.2 | 75 21 AAY68529 | Synthetic foot and |
| 27 | 75 | 74.3 | 35 7 AAP60895 | Peptide containing |
| 28 | 75 | 74.3 | 35 9 AAP82746 | VPI(A12,119) contg |
| 29 | 71 | 70.3 | 35 21 AAY68508 | Consensus antigen |
| 30 | 71 | 70.3 | 213 4 AAP30198 | Sequence encoded b |
| 31 | 71 | 70.3 | 233 4 AAP30209 | Sequence of antige |
| 32 | 70 | 69.3 | 18 4 AAP30110 | Sequence of VPI ca |
| 33 | 67 | 66.3 | 20 5 AAP40103 | Sequence at antige |
| 34 | 67 | 66.3 | 216 5 AAP40085 | Sequence of foot a |
| 35 | 64 | 63.4 | 248 4 AAP30207 | Sequence of an FMD |
| 36 | 63 | 62.4 | 35 21 AAY68509 | Consensus antigen |
| 37 | 63 | 62.4 | 55 21 AAY68533 | Synthetic foot and |
| 38 | 58 | 57.4 | 218 4 AAP30196 | Sequence encoded b |
| 39 | 56 | 55.4 | 28 4 AAP30316 | Sequence of VPI ca |
| 40 | 56 | 55.4 | 213 21 AAB15428 | FMDV antigen for r |
| 41 | 56 | 55.4 | 213 21 AAB15397 | Foot-and-mouth dis |
| 42 | 56 | 55.4 | 213 21 AAB15398 | Foot-and-mouth dis |
| 43 | 56 | 55.4 | 213 21 AAB15402 | Foot-and-mouth dis |
| 44 | 54 | 53.5 | 36 7 AAP60896 | Peptide containing |
| 45 | 54 | 53.5 | 36 9 AAP82747 | VPI(A24,C) contg. |

ALIGNMENTS

| | |
|----------|--|
| RESULT 1 | ABU08643 |
| ID | ABU08643 standard; peptide; 19 AA. |
| XX | |
| AC | ABU08643: |
| XX | |
| DT | 04-JUN-2003 (first entry) |
| XX | |
| DE | Foot and mouth disease virus (FMDV) VPI-A12141-159, variant FL. |
| XX | |
| KW | Foot and mouth disease virus; FMDV; VPI-A12 region; immunosuppressive; |
| KW | antidiabetic; antianaemic; neuroprotective; vaccine; |
| KW | anti-metallothionein antibody; humoral immune response; |
| KW | autoimmune disease; Grave's disease; rheumatoid arthritis; |
| KW | systemic lupus erythematosus; Type 1 diabetes; pernicious anaemia; |
| KW | multiple sclerosis; Sjorgen's disease. |
| XX | |
| OS | Foot and mouth disease virus. |
| XX | |
| PN | US2003007973-A1. |
| XX | |
| PD | 09-JAN-2003. |
| XX | |
| PF | 24-JUN-2002; 2002US-0178909. |
| XX | |
| PR | 22-JUN-2001; 2001US-300346P. |
| XX | |
| PA | (LYNE/) LYNES M. A. |
| PI | Lynes MA; |
| XX | |

DR WPI; 2003-353082/33.
XX
XX Treating autoimmune diseases, e.g. Grave's disease, arthritis, lupus,
PT or diabetes by administering a composition consisting of an
PT anti-metallothionein antibody to stimulate a humoral immune response in
PT a subject -
XX
XX Example 7; Fig 9; 24pp; English.
XX
XX The invention describes a method of treating a subject comprising
CC administering to the subject a composition consisting of an
CC anti-metallothionein antibody to stimulate a humoral immune response in
CC a subject. The methods and compositions are useful for treating
CC autoimmune diseases, e.g. Grave's disease, rheumatoid arthritis,
CC systemic lupus erythematosus, Type 1 diabetes, pernicious anaemia,
CC multiple sclerosis or Sjorgen's disease. This is the amino acid
CC sequence of foot and mouth disease virus (FMDV) VP1-A12141-159 region
CC used as an immunogen.
XX
XX
SQ Sequence 19 AA;
Query Match 91.1%; Score 92; DB 24; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GSGVRGDFGSLARVARQL 20
DB 1 GSGVRGDFGSLARVARQL 19
RESULT 2
ABU08642
ID ABU08642 standard; peptide: 19 AA.
XX
XX ABU08642;
AC
XX
XX 04-JUN-2003 (first entry)
DT
XX
XX Foot and mouth disease virus (FMDV) VP1-A12141-159, variant FP.
DE
XX
XX Foot and mouth disease virus; FMDV; VP1-A12 region; immunosuppressive;
KW antiinflammatory; antiarthritic; antirheumatic; dermatological;
KW antidiabetic; antinaemic; neuroprotective; vaccine;
KW anti-metallothionein antibody; humoral immune response;
KW autoimmune disease; Grave's disease; rheumatoid arthritis;
KW systemic lupus erythematosus; Type 1 diabetes; pernicious anaemia;
XX multiple sclerosis; Sjorgen's disease.
XX
XX Foot and mouth disease virus.
OS
XX
XX US2003007973-A1.
PN
XX
XX 09-JAN-2003.
PD
XX
XX 24-JUN-2002; 2002US-0178909.
PF
XX
XX 22-JUN-2001; 2001US-300346P.
PR
XX
XX (LYNE/) LYNES M A.
PA
XX
XX Lynes MA;
PI
XX
XX WPI; 2003-353082/33.
DR
XX
XX Treating autoimmune diseases, e.g. Grave's disease, arthritis, lupus,
PT or diabetes by administering a composition consisting of an
PT anti-metallothionein antibody to stimulate a humoral immune response in
PT a subject -
XX
XX Example 7; Fig 9; 24pp; English.
XX
XX The invention describes a method of treating a subject comprising
CC administering to the subject a composition consisting of an

CC anti-metallothionein antibody to stimulate a humoral immune response in
CC a subject. The methods and compositions are useful for treating
CC autoimmune diseases, e.g. Grave's disease, rheumatoid arthritis,
CC systemic lupus erythematosus, Type 1 diabetes, pernicious anaemia,
CC multiple sclerosis or Sjorgen's disease. This is the amino acid
CC sequence of foot and mouth disease virus (FMDV) VP1-A12141-159 region
CC used as an immunogen.
XX
XX
SQ Sequence 19 AA;
Query Match 84.2%; Score 85; DB 24; Length 19;
Best Local Similarity 94.7%; Pred. No. 4.2e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GSGVRGDFGSLARVARQL 20
DB 1 GSGVRGDFGSLARVARQL 19
RESULT 3
AA94587
ID AA94587 standard; Peptide: 20 AA.
XX
XX AA94587;
AC
XX
XX 10-JAN-2001 (first entry)
DT
XX
XX Envelope gene epitope of foot and mouth disease virus.
DE
XX
XX Hepatitis B virus nucleocapsid antigen; HBcAg; T cell epitope;
KW cytolytic T lymphocyte; immunogenic; ICE; CTL; FMDV;
KW immunodominant core epitope; immunisation; envelope gene.
XX
XX Foot and mouth disease virus.
OS
XX
XX WO200026385-A1.
PN
XX
XX 11-MAY-2000.
PD
XX
XX 05-NOV-1999; 99WO-US26291.
PF
XX
XX 05-NOV-1998; 98US-0107169.
PR
XX
XX (POWD-) POWDERJECT VACCINES INC.
PA
XX
XX Fuller DL, Fuller JT;
PI
XX
XX WPI; 2000-451623/39.
DR
XX
XX Use of expression vector for nucleic acid immunization that comprises
PT promoter and recombinant nucleic acid sequences encoding Hepatitis B
PT core antigen and T cell epitope from antigen -
PT core antigen and T cell epitope from antigen -
XX
XX Example 6; Page 39; 55pp; English.
PS
XX
XX The present invention relates to an immunogenic recombinant
CC nucleic acid molecule. The molecule consists of a modified hepatitis
CC B virus nucleocapsid antigen (HBcAg) with a T cell epitope sequence
CC inserted within the HBcAg. The creation of a unique restriction site
CC in HBcAg facilitated the insertion of the T cell epitope into the DNA
CC encoding the immunodominant core epitope of the HBcAg. An example of a
CC suitable insertion epitope is the present sequence, the
CC neutralisation epitope from the foot and mouth disease virus envelope
CC gene. Alternatively other T cell epitopes may be inserted
CC (AA94583, AA94584, AA94585, AA94586, AA94588). The recombinant
CC nucleic acid molecule may then be used as a reagent in various nucleic
CC acid immunisation strategies. The advantage of this method of
CC immunisation is that the nucleic acid reagents that encode hybrid HBcAg
CC generate an extremely high frequency cellular immune response against
CC the CTL epitope.
XX
XX Sequence 20 AA;

Query Match 84.2%; Score 85; DB 21; Length 20;
 Best Local Similarity 94.7%; Pred. No. 4.5e-06;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 2 GSGVGRDGFSLAPRVARQL 20
 DB 1 GSGVGRDGFSLAPRVARQL 19

RESULT 4
 AAP30107
 ID AAP30107 standard; Peptide: 31 AA.
 AC AAP30107;
 XX
 XX 03-APR-1992 (first entry)
 DT
 XX Sequence of VP1 capsid protein residues 130-160 from the amino-
 DE terminus, FMDV, Tudinggen type A, subtype 12, strain 119.
 XX
 KM Antigen; Picornavirus; capsid protein; antibody; detection;
 KW vaccine; diagnosis.
 XX
 OS Foot and mouth disease virus.
 XX
 PN WO8303547-A.
 XX
 PD 27-OCT-1983.
 XX
 PF 14-APR-1983; 83WO-0002644.
 XX
 XX 25-MAR-1983; 83US-0478847.
 PR 14-APR-1982; 82US-0368308.
 PR 20-SEP-1984; 84US-0653475.
 PR 18-DEC-1984; 84US-0682819.
 XX
 XX (BITTLE) BITTLE J L.
 PA (SCRI-) SCRIPPS CLINIC & RE.
 XX
 PI Bitttle JL, Lerner RA;
 XX
 DR WPI; 1983-807942/44.
 XX
 PT Antigenic peptide(s) corresp. to picornavirus capsid protein -
 PT useful in prodn. of vaccines and in diagnostic tests
 XX
 XX Example; Page 26; 90pp; English.
 PS
 XX The peptides of the invention corresp. to a region on the antigenic
 CC Picornavirus capsid protein. The capsid protein FMDV VP1 or polio
 CC virus VP1. When linked to carriers the peptides are immunogenic.
 CC Dose is 20 ug-2mg peptide for inoculations.
 XX
 SQ Sequence 31 AA;
 Query Match 84.2%; Score 85; DB 4; Length 31;
 Best Local Similarity 94.7%; Pred. No. 6.8e-06;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 2 GSGVGRDGFSLAPRVARQL 20
 DB 11 GSGVGRDGFSLAPRVARQL 29

XX
 XX Foot-and-mouth disease; vaccine; antigen;
 KW
 XX Foot-and-mouth disease virus.
 OS
 XX US4544500-A.
 PN
 XX 01-OCT-1985.
 PD
 XX 18-DEC-1984; 84US-0682819.
 PF
 XX 18-DEC-1984; 84US-0682819.
 PR 18-DEC-1984; 84US-0682819.
 XX
 XX (SCRI-) SCRIPPS CLINIC & RESEARCH FOUNDATION.
 PA
 XX Bitttle JL, Lerner RA;
 PI
 XX WPI; 1985-262823/42.
 DR
 XX Synthetic foot and mouth disease antigen - comprising 20 amino acid
 PT peptide corresp. to virus protein VP1.
 PT
 XX Disclosure; page 4; 7pp; English.
 PS
 XX The peptide corresponds to amino acids 130-160 of the foot and mouth
 CC disease virus VP1 protein. It represents a monospecific synthetic
 CC antigenic determinant. The peptide can be used to vaccinate animals,
 CC esp. swine and cattle, against the virus with a single inoculation.
 XX
 SQ Sequence 31 AA;
 Query Match 84.2%; Score 85; DB 6; Length 31;
 Best Local Similarity 94.7%; Pred. No. 6.8e-06;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 2 GSGVGRDGFSLAPRVARQL 20
 DB 11 GSGVGRDGFSLAPRVARQL 29

RESULT 6
 AAW17082
 ID AAW17082 standard; peptide: 31 AA.
 XX
 AC AAW17082;
 XX
 XX 13-JUN-1997 (first entry)
 DT
 XX Foot and mouth disease virus G-H loop of protein VP-1.
 DE
 XX Foot and mouth disease; aphthovirus; vaccine; antigen; epitope;
 KW immunogen; G-H loop; VP-1; deletion; mutant; binding site removal;
 KW antibody; non-infectious; attenuated.
 XX
 OS Foot and mouth disease virus.
 OS
 XX US5612040-A.
 PN
 XX 18-MAR-1997.
 PD
 XX 07-APR-1995; 95US-0418716.
 PF
 XX 07-APR-1995; 95US-0418716.
 PR 07-APR-1995; 95US-0418716.
 XX
 XX (USDA) US SEC OF AGRIC.
 PA
 XX Baxt B, Berinstein A, Kang AS, Mason PW, Reider E;
 PI WPI; 1997-192081/17.
 DR
 XX Genetically modified foot-and-mouth disease virus - lacks
 PT cell-binding site and is non-infectious, useful in vaccines
 XX

PS Disclosure; Figure 1; 10pp; English.

XX CC AAM17082 represents amino acids 130-163 of wild-type foot and mouth
 CC disease (FMD) virus VP-1 structural protein. The sequence represents
 CC the G-H loop, a flexible loop between the G and H beta strands of VP-1.
 CC The G-H loop is the main antigenic site of VP-1 and is also involved in
 CC cell binding. The FMD virus G-H loop peptide can be modified in a FMD
 CC virus by deletion of the amino acid (aa) sequence
 CC Gly-Val-Arg-Gly-Asp-Phe (aa 142-147) and replacing this sequence with the
 CC sequence Asn-Pro. This results in the virus retaining its immunogenicity
 CC but is not infectious because the cell binding site has been removed. The
 CC genetically modified FMD virus is useful in vaccines against the
 CC disease.

XX SQ Sequence 31 AA;

Query Match 84.2%; Score 85; DB 18; Length 31;
 Best Local Similarity 94.7%; Pred. No. 6.Be-06;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GSGVGRDPSGLAPRVARQL 20
 |||||
 DB 11 GSGVGRDPSGLAPRVARQL 29

RESULT 7
 AAY68501
 ID AAY68501 standard; peptide; 35 AA.
 XX AAY68501;
 AC
 XX 05-MAY-2000 (first entry)
 DT
 XX Target antigenic peptide derived from amino acids 134-169 of VP1.
 DE
 XX Antigenic peptide; VP1 capsid protein; FMDV strain A12; epitope;
 KW helper T-cell epitope; immune response; vaccine; FMDV infection.
 KM
 XX Foot and mouth disease virus.
 OS
 XX WO9966954-A1.
 PN
 XX 29-DEC-1999.
 PD
 XX 21-JUN-1999; 99WO-US13921.
 PF
 XX 20-JUN-1998; 98US-0100600.
 PR
 XX (UNBI-) UNITED BIOMEDICAL INC.
 PA
 XX Wang CY, Shen M;
 PI
 XX WPI; 2000-160563/14.
 DR
 XX Synthetic peptide used in protecting animals against Foot-and-Mouth
 PT Disease Virus infections comprises a helper T-cell epitope and a
 PT Foot-and-Mouth Disease Virus epitope conjugate -
 PT
 XX Claim 1; Page 45; 115pp; English.

XX The present sequence represents a target antigenic peptide derived from
 CC the VP1 capsid protein of Foot and Mouth Disease Virus (FMDV) strain A12.
 CC The peptide is used to design synthetic epitopes, which are conjugated
 CC to a helper T-cell epitope and optionally an immunostimulator sequence.
 CC The peptides are covalently linked to each other, preferably by peptide
 CC bonds generated through direct synthesis. The synthetic vaccines of the
 CC invention require lower levels of biosecurity. The synthetic vaccines of the
 CC immunogenic activity, are less prone to product instability and
 CC lot-to-lot variability and do not need periodic revision due to
 CC antigenic variation in the field. The peptides are used as immunogens
 CC in vaccines to generate an enhanced immune response against a FMDV
 CC antigen in animals, such as swine, cattle, sheep, goats and susceptible
 CC wild species. They can also be used to diagnose FMDV infection in a

CC mammal.

XX SQ Sequence 35 AA;

Query Match 84.2%; Score 85; DB 21; Length 35;
 Best Local Similarity 94.7%; Pred. No. 7.6e-06;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GSGVGRDPSGLAPRVARQL 20
 |||||
 DB 7 GSGVGRDPSGLAPRVARQL 25

RESULT 8
 AAY68528
 ID AAY68528 standard; peptide; 75 AA.
 XX AAY68528;
 AC
 XX 05-MAY-2000 (first entry)
 DT
 XX Synthetic foot and mouth disease virus immunogen.
 DE
 XX Antigenic peptide; VP1 capsid protein; serotype Asia; epitope;
 KW helper T-cell epitope; immune response; vaccine; FMDV infection.
 KM
 XX Synthetic.
 OS
 XX Foot and mouth disease virus.
 OS
 XX
 XX Key Location/Qualifiers
 FT Peptide 1..16
 FT /note- "Yersinia Invasin domain (immunostimulator
 FT peptide"
 FT Peptide 17..18
 FT /note- "spacer"
 FT Peptide 19..38
 FT /note- "autologous helper T-cell epitope derived
 FT from VP1 capsid protein"
 FT Peptide 39..40
 FT /note- "spacer"
 FT Peptide 41..75
 FT /note- "synthetic VP1 capsid protein epitope"
 FT
 XX WO9966954-A1.
 PN
 XX 29-DEC-1999.
 PD
 XX 21-JUN-1999; 99WO-US13921.
 PF
 XX 20-JUN-1998; 98US-0100600.
 PR
 XX (UNBI-) UNITED BIOMEDICAL INC.
 PA
 XX Wang CY, Shen M;
 PI
 XX WPI; 2000-160563/14.
 DR
 XX Synthetic peptide used in protecting animals against Foot-and-Mouth
 PT Disease Virus infections comprises a helper T-cell epitope and a
 PT Foot-and-Mouth Disease Virus epitope conjugate -
 PT
 XX Claim 8; Page 96; 115pp; English.

XX The present sequence represents a foot and mouth disease (FMDV) vaccine
 CC antigen of the invention. The specification describes epitopes derived from an
 CC antigen of the VP1 capsid protein of FMDV. The VP1 epitopes are
 CC conjugated to a helper T-cell epitope and optionally an immunostimulator
 CC sequence. The peptides are covalently linked to each other, preferably
 CC by peptide bonds generated through direct synthesis. The synthetic
 CC vaccines of the invention require lower levels of biosecurity, have a
 CC reduced loss of immunogenic activity, are less prone to product
 CC instability and lot-to-lot variability and do not need periodic revision

CC due to antigenic variation in the field. The peptides are used as
CC immunogens in vaccines to generate an enhanced immune response against
CC a FMDV antigen in animals, such as swine, cattle, sheep, goats and
CC susceptible wild species. They can also be used to diagnose FMDV
CC infection in a mammal.

SO Sequence 75 AA;

Query Match 84.2%; Score 85; DB 21; Length 75;
Best Local Similarity 94.7%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GSGVRGDFGSLAPRVAROL 20
DB 47 GSGVRGDFGSLAPRVAROL 65
|||||

RESULT 9
AAP30205
ID AAP30205 standard; Protein; 216 AA.

AC AAP30205;

XX 29-JUL-1992 (first entry)

DE Sequence encoded by direct expression vector pFM 10 which
DE comprises the promoter and operator of the E. coli cryptophan
DE operon Aas 1-211 of the VP3 gene linked to 4 AAs from pBR322.

XX Vaccine; immunogen; antigen; viral protein.

OS Foot and mouth disease virus.

XX EP68693-A.

PD 05-JAN-1983.

XX 11-JUN-1982; 82EP-0303040.

XX 04-MAY-1982; 82US-0374855.

PR 16-JUN-1981; 81US-0274103.

XX (GETH) GENENTECH INC.

XX Kield DG, Yansura DG;

XX WPI; 1983-05055K/03.

DR N-PSDB; AAN30144.

PT recombinant DNA technology for vaccine prodn.
XX Example: Page 36-37; 81pp; English.

CC The inventors claim a polypeptide comprising at least one antigen of
CC FMDV, or a fusion polypeptide of at least two antigens from at least
CC two different FMDV strands, and encoding DNA. Pref. the fusion
CC polypeptide has the sequence of two of the A, C, O, Asia-1, SAT 1,
CC SAT 2 and SAT 3 type strains of the virus. The polypeptides pref.
CC comprise Aas 55-177 or 1-210 of the VP3 virus. Fusion polypeptides
CC may comprise Aas 1-210 fused to 8-210 of VP3 virus protein. pFM1,
CC pFM2, pFM3, pFM10, pFM20, pFM31, pFMC, pFMD, pFMF and pFMG are also
CC claimed.

SO Sequence 216 AA;

Query Match 84.2%; Score 85; DB 4; Length 216;
Best Local Similarity 94.7%; Pred. No. 4.4e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GSGVRGDFGSLAPRVAROL 20
DB 141 GSGVRGDFGSLAPRVAROL 159
|||||

RESULT 10
AAP30195
ID AAP30195 standard; Protein; 220 AA.

AC AAP30195;

XX 29-JUL-1992 (first entry)

DE Sequence encoded by VP3 gene of FMDV type A12 (T465).

XX Vaccine; immunogen; antigen; viral protein.

OS Foot and mouth disease virus.

XX EP68693-A.

PD 05-JAN-1983.

XX 11-JUN-1982; 82EP-0303040.

XX 04-MAY-1982; 82US-0374855.

PR 16-JUN-1981; 81US-0274103.

XX (GETH) GENENTECH INC.

XX Kield DG, Yansura DG;

XX WPI; 1983-05055K/03.

DR N-PSDB; AAN30127.

PT polypeptide antigens of foot-and-mouth disease - obtd. by
PT recombinant DNA technology for vaccine prodn.

XX Disclosure; Fig 2; 81pp; English.

CC The inventors claim a polypeptide comprising at least one antigen of
CC FMDV, or a fusion polypeptide of at least two antigens from at least
CC two different FMDV strands, and encoding DNA. Pref. the fusion
CC polypeptide has the sequence of two of the A, C, O, Asia-1, SAT 1,
CC SAT 2 and SAT 3 type strains of the virus. The polypeptides pref.
CC comprise Aas 55-177 or 1-210 of the VP3 virus. Fusion polypeptides
CC may comprise Aas 1-210 fused to 8-210 of VP3 virus protein. pFM1,
CC pFM2, pFM3, pFM10, pFM20, pFM31, pFMC, pFMD, pFMF and pFMG are also
CC claimed.

SO Sequence 220 AA;

Query Match 84.2%; Score 85; DB 4; Length 220;
Best Local Similarity 94.7%; Pred. No. 4.4e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GSGVRGDFGSLAPRVAROL 20
DB 140 GSGVRGDFGSLAPRVAROL 158
|||||

RESULT 11
AAP30204
ID AAP30204 standard; Protein; 233 AA.

AC AAP30204;

XX 29-JUL-1992 (first entry)

DE Sequence encoded by pFM3 which comprises 17 AAs from the LE' gene
DE construction (fragment 3a), linked to a methionine AA (CNR cleavable),
DE linked to the Aas 1-211 of the VP3 FMDV A12, linked to 4 AAs from
DE pBR322.

XX Vaccine; immunogen; antigen; viral protein.

```

OS Foot and mouth disease virus and Escherichia coli.
PN EP63693-A.
PD 05-JAN-1983.
XX
XX 11-JUN-1982; 82EP-0303040.
XX
XX 04-MAY-1982; 82US-0374855.
PR 16-JUN-1981; 81US-0274103.
XX
XX (GETH ) GENENTECH INC.
XX
XX Kfield DG, Yansura DG;
XX WPI; 1983-05055K/03.
DR N-PSDB; AAN30142.
XX
XX Polypeptide antigens of foot-and-mouth disease - obtd. by
PT recombinant DNA technology for vaccine prodn.
XX
XX Example; Page 33-34; 81pp; English.
XX
XX The inventors claim a polypeptide comprising at least one antigen of
CC FMDV, or a fusion polypeptide of at least two antigens from at least
CC two different FMDV strands, and encoding DNA. Pref. the fusion
CC polypeptide has the sequence of two of the A, C, O, Asia-1, SAT 1,
CC SAT 2, and SAT 3 type strains of the virus. The polypeptides pref.
CC comprise AAs 55-177 or 1-210 of the VP3 virus. Fusion polypeptides
CC may comprise AAs 1-210 fused to 8-210 of VP3 virus protein. PFML,
CC PFM2, PFM3, PFML0, PFM20, PFML1, PFMC, PFMD, PFMF and PFMG are also
CC claimed.
XX
XX Sequence 233 AAs;
SQ
XX
XX Query Match 84.2%; Score 85; DB 4; Length 233;
XX Best Local Similarity 94.7%; Pred. No. 4.7e-05;
XX Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
QY 2 GSGVGRDGFSLALRVARQL 20
XX |||||||
Db 158 GSGVGRDGFSLAPRVARQL 176
XX
XX RESULT 12
XX AAP30202
XX ID AAP30202 standard; Protein; 405 AA.
XX
XX AAP30202;
AC
XX 29-JUL-1992 (first entry)
DT
XX
XX Sequence encoded by PFML which comprises 190 AAs form the LE' gene
DE construction linked to 6 AAs from the linker molecule (fragment 4),
DE linked to 205 AAs from the VP3 FMDV A12 (codons 7-211), linked to
DE 4 AAs from pBR322.
XX
XX Vaccine; Immunogen; antigen; viral protein.
KW
XX
XX Foot and mouth disease virus and Escherichia coli.
OS
XX
XX EPE68693-A.
PN
XX
XX 05-JAN-1983.
PD
XX
XX 11-JUN-1982; 82EP-0303040.
PE
XX
XX 04-MAY-1982; 82US-0374855.
PR 16-JUN-1981; 81US-0274103.
XX
XX (GETH ) GENENTECH INC.
PA
XX
XX Kfield DG, Yansura DG;
PI

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```

XX DR WPI: 1983-05055K/03.
XX DR N-PSDB; AAN30140.
XX PT Polypeptide antigens of foot-and-mouth disease - obt'd. by
XX XX recombinant DNA technology for vaccine prodn.
XX PS Example; Page 29-31; 81pp; English.
XX
CC CC The inventors claim a polypeptide comprising at least one antigen of
CC CC FMDV, or a fusion polypeptide of at least two antigens from at least
CC CC two different FMDV strands, and encoding DNA. Pref. the fusion
CC CC polypeptide has the sequence of two of the A, C, O, Asia-1, SAT 1,
CC CC SAT 2 and SAT 3 type strains of the virus. The polypeptides pref.
CC CC comprise AAs 55-177 or 1-210 of the VP3 virus. Fusion polypeptides
CC CC may comprise AAs 1-210 fused to 8-210 of VP3 virus protein. pFM1,
CC CC pFM2, pFM3, pFM10, pFM20, pFM11, pFMC, pFMD, pFMF and pFMG are also
CC CC claimed.
XX
SQ Sequence 405 AA;
OY 2 GSGVGRDGSIALRVARQL 20
Db 330 GSGVGRDGSIALRVARQL 348
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 13
AAP30203
ID AAP30203 standard; Protein; 406 AA.
AC AAP30203;
XX
DT 29-JUL-1992 (first entry)
DE Sequence encoded by pFM2 which comprises 190 AAs from the LE' gene,
DE linked to a methionine AA (CNR cleavable), linked to the AAs 1-211
DE of the VP3 FMDV A12 (codons 1-7 are derived from synthetic DNA, 8-211
DE are natural codons), linked to 4 amino acids from pBR322.
XX
KW Vaccine; immunogen; antigen; viral protein.
OS Foot and mouth disease virus and Escherichia coli.
XX
XX EP68693-A.
XX PN 05-JAN-1983.
XX PD 11-JUN-1982; 82EP-0303040.
XX PF 04-MAY-1982; 82US-0374855.
XX PR 16-JUN-1981; 81US-0274103.
XX
XX (GETH ) GENENTECH INC.
XX
XX K1eld DG; Yansura DG;
XX
XX WPI: 1983-05055K/03.
XX DR N-PSDB; AAN30141.
XX
XX Polypeptide antigens of foot-and-mouth disease - obt'd. by
XX XX recombinant DNA technology for vaccine prodn.
XX PS Example; Page 31-32; 81pp; English.
XX
CC CC The inventors claim a polypeptide comprising at least one antigen of
CC CC FMDV, or a fusion polypeptide of at least two antigens from at least
CC CC two different FMDV strands, and encoding DNA. Pref. the fusion
CC CC polypeptide has the sequence of two of the A, C, O, Asia-1, SAT 1,
CC CC SAT 2 and SAT 3 type strains of the virus. The polypeptides pref.

```

CC comprise AAs 55-177 or 1-210 of the VP3 virus. Fusion polypeptides
CC may comprise AAs 1-210 fused to 8-210 of VP3 virus protein. pFM1,
CC pFM2, pFM3, pFM10, pFM20, pFM31, pFM4, pFM5, pFM6 and pFM7 are also
CC claimed.

XX Sequence 406 AA;

Query Match 84.2%; Score 85; DB 4; Length 406;
Best Local Similarity 94.7%; Pred. No. 8e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GSGVGDGSLALRVAROL 20
|||||

DB 331 GSGVGDGSLALRVAROL 349

RESULT 14

AAP30206 ID AAP30206 standard; Protein; 609 AA.

XX AAP30206;

XX 29-JUL-1992 (first entry)

DE Sequence encoded by pFM 20 which is the polyanthigen comprising 190 AAs
DE coded by the IE' gene construction, linked to a methionine AA (CMB
DE cleavable), linked to the AAs 1-211 of the VP3 FMDV A12 (codons 1-7
DE are derived from synthetic DNA), linked to AAs 8-211 of the VP3
DE FMDV A12, linked to 4 AAs from pBR322.

XX Vaccine; immunogen; antigen; viral protein.

XX Foot and mouth disease virus and Escherichia coli.

XX EPE8693-A.

XX 05-JAN-1983.

XX 11-JUN-1982; 82EP-0303040.

XX 04-MAY-1982; 82US-0374855.

PR 16-JUN-1981; 81US-0274103.

XX (GETH) GENENTECH INC.

XX Kleid DG, Yansura DG;

XX WPI; 1983-05055K/03.

DR N-PSDB; AAN30145.

XX Polypeptide antigens of foot-and-mouth disease - obtd. by

PT recombinant DNA technology for vaccine prodn.

XX Example; Page 38-41; 81pp; English.

CC The inventors claim a polypeptide comprising at least one antigen of
CC FMDV, or a fusion polypeptide of at least two antigens from at least
CC two different FMDV strands, and encoding DNA. Pref. the fusion
CC polypeptide has the sequence of two of the A, C, O, Asia-1, SAT 1,
CC SAT 2 and SAT 3 type strains of the virus. The polypeptides pref.
CC comprise AAs 55-177 or 1-210 of the VP3 virus. Fusion polypeptides
CC may comprise AAs 1-210 fused to 8-210 of VP3 virus protein. pFM1,
CC pFM2, pFM3, pFM10, pFM20, pFM31, pFM4, pFM5, pFM6 and pFM7 are also
CC claimed.

XX Sequence 609 AA;

Query Match 84.2%; Score 85; DB 4; Length 609;
Best Local Similarity 94.7%; Pred. No. 0.00012;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GSGVGDGSLALRVAROL 20
|||||

DB 331 GSGVGDGSLALRVAROL 349

RESULT 15

AAR38543 ID AAR38543 standard; peptide; 20 AA.

XX AAR38543;

XX 25-MAR-2003 (updated)

DT 11-JAN-1994 (first entry)

XX Foot and Mouth Disease Virus VPI antigenic peptide.

XX Multivalent vaccine; polyllysine; homopolymer; dendritic core;
XX multiple antigen peptide system; MAPS; Foot and Mouth Disease;
XX FMDV; VPI protein; Aphthovirus; vaccine.

XX Foot and Mouth Disease Virus.

XX US5229490-A.

XX 20-JUL-1993.

XX 20-DEC-1990; 90US-0631185.

XX 06-MAY-1987; 87US-0047204.

XX 30-JUN-1987; 87US-0068840.

XX 12-APR-1989; 89US-0336845.

XX 20-DEC-1990; 90US-0631185.

XX (UYRQ) UNIV ROCKEFELLER.

XX Tam JP;

XX WPI; 1993-242534/30.

XX Multiple antigenic peptide systems - have dendritic core attached

XX covalently to antigens, used as vaccine

XX Claim 26; Column 24; 23pp; English.

XX This is a preferred FMDV antigenic peptide suitable for

XX construction of a Multiple Antigen Peptide System (MAPS) by

XX covalent coupling to a dendritic homopolymer core (esp.

XX polyllysine). The antigen is derived from the Foot and Mouth Disease

XX Virus VPI protein.

XX (updated on 25-MAR-2003 to correct PF field.)

XX Sequence 20 AA;

Query Match 83.2%; Score 84; DB 14; Length 20;
Best Local Similarity 94.7%; Pred. No. 6.3e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GSGVGDGSLALRVAROL 20
|||||

DB 1 GSGVGDGSLALRVAROL 19

Search completed: October 9, 2003, 10:14:18
Job time : 58.3333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 10:10:09 ; Search time 19.6667 Seconds
(without alignments)
97.799 Million cell updates/sec

Title: US-09-549-186b-8

Perfect score: 101

Sequence: 1 CGSGVRGDFGSLARVARQL 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR_76:*
2: p1r1:*
3: p1r2:*
4: p1r3:*
5: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 85 | 84.2 | 2332 | 1 GNNY4F | genome polyprotein |
| 2 | 67 | 66.3 | 216 | 2 A03911 | genome polyprotein |
| 3 | 50 | 49.5 | 230 | 2 A03909 | genome polyprotein |
| 4 | 50 | 49.5 | 2336 | 2 S37077 | genome polyprotein |
| 5 | 48 | 47.5 | 354 | 2 F90965 | hypothetical prote |
| 6 | 48 | 47.5 | 564 | 2 F85813 | hypothetical prote |
| 7 | 48 | 47.5 | 569 | 2 H64959 | probable membrane |
| 8 | 48 | 47.5 | 2333 | 1 GNNY2F | ribosomal protein |
| 9 | 47 | 46.5 | 170 | 2 T35564 | genome polyprotein |
| 10 | 45 | 44.6 | 109 | 2 S61252 | genome polyprotein |
| 11 | 45 | 44.6 | 109 | 2 S61253 | genome polyprotein |
| 12 | 44 | 43.6 | 76 | 2 D82844 | carbon storage reg |
| 13 | 44 | 43.6 | 303 | 2 E72463 | hypothetical prote |
| 14 | 44 | 43.6 | 505 | 2 S44647 | f42h10.1 protein - |
| 15 | 44 | 43.6 | 532 | 2 S23355 | alpha-amylase (EC |
| 16 | 44 | 43.6 | 537 | 2 AB1869 | type I site-specif |
| 17 | 43.5 | 43.1 | 429 | 2 S43459 | TOM34 protein - ye |
| 18 | 43 | 42.6 | 39 | 2 I49418 | insulin I precursor |
| 19 | 43 | 42.6 | 108 | 1 INMS1 | hypothetical prote |
| 20 | 43 | 42.6 | 260 | 2 B64563 | translation elonga |
| 21 | 43 | 42.6 | 281 | 1 S34626 | TRADD protein - hu |
| 22 | 43 | 42.6 | 312 | 2 A56911 | protochlorophyllid |
| 23 | 43 | 42.6 | 400 | 2 S20941 | outer membrane hem |
| 24 | 43 | 42.6 | 681 | 2 E82812 | IcmF [imported] - |
| 25 | 43 | 42.6 | 1159 | 2 AH3088 | hypothetical prote |
| 26 | 43 | 42.6 | 1159 | 2 B98198 | genome polyprotein |
| 27 | 43 | 42.6 | 2205 | 1 GNNY2M | genome polyprotein |
| 28 | 43 | 42.6 | 2207 | 1 GNNY5P | genome polyprotein |
| 29 | 43 | 42.6 | 2207 | 2 S09553 | genome polyprotein |

| | | | | | |
|----|------|------|------|----------|---------------------|
| 30 | 42 | 41.6 | 110 | 1 IPRT1 | insulin 1 precursor |
| 31 | 42 | 41.6 | 173 | 2 T11545 | NADH2 dehydrogenas |
| 32 | 42 | 41.6 | 173 | 2 T11311 | NADH2 dehydrogenas |
| 33 | 42 | 41.6 | 291 | 2 T37992 | probable tricarbox |
| 34 | 42 | 41.6 | 309 | 2 H71328 | probable flagellar |
| 35 | 42 | 41.6 | 331 | 2 E82389 | probable outer mem |
| 36 | 42 | 41.6 | 350 | 1 S52153 | alcohol dehydrogen |
| 37 | 42 | 41.6 | 467 | 2 B75322 | probable oligoendo |
| 38 | 42 | 41.6 | 486 | 1 KRXL | keratin 3, type I, |
| 39 | 42 | 41.6 | 1381 | 2 S55619 | capsid protein 25 |
| 40 | 41.5 | 41.1 | 110 | 1 IPRT2 | insulin 2 precursor |
| 41 | 41.5 | 41.1 | 570 | 2 B86827 | hypothetical prote |
| 42 | 41 | 40.6 | 136 | 2 H90573 | ribosomal protein |
| 43 | 41 | 40.6 | 229 | 2 AD2462 | hypothetical prote |
| 44 | 41 | 40.6 | 236 | 2 E69479 | conserved hypothet |
| 45 | 41 | 40.6 | 289 | 2 A87534 | carboxylesterase f |

ALIGNMENTS

RESULT 1

GNNY4F

genome polyprotein - foot-and-mouth disease virus A (strain A12)
N:Contains: coat protein VP1; coat protein VP2; coat protein VP3; coat protein VP4; c
tein VPg2; genome-linked protein VPg3; nonstructural protein p20a; proteinase (EC 3.4
C:Species: Aphthovirus A (foot-and-mouth disease virus A)
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
C:Accession: A25794

R:Robertson, B.H.; Grubman, M.J.; Weddell, G.N.; Moore, D.M.; Welsh, J.D.; Fischer, T

J. Virol. 54, 651-660, 1985
A:Title: Nucleotide and amino acid sequence coding for polypeptides of foot-and-mouth

A:Reference number: A25794; NUID:85211015; PMID:2987518
A:Accession: A25794

A:Molecule type: genomic RNA
A:Residues: 12332 <ROB>

A:Cross-references: GB:M10975; NID:g210306; PIDN:AAA42593.1; PID:g210307
C:Superfamily: foot-and-mouth disease virus genome polyprotein

C:Keywords: coat protein; core protein; genome-linked protein; hydrolase; nonstructur

F:1-216/Product: nonstructural protein p20a #status predicted <RPA>
F:217-285/Product: coat protein VP4 #status predicted <VP4> *

F:286-503/Product: coat protein VP2 #status predicted <VP2>
F:504-723/Product: coat protein VP3 #status predicted <VP3>

F:724-937/Product: coat protein VP1 #status predicted <VP1>
F:938-953/Product: core protein X #status predicted <CPX>

F:954-1107/Product: core protein p14 #status predicted <C14>
F:1108-1425/Product: core protein p41 #status predicted <C41>

F:1426-1578/Product: core protein p19 #status predicted <C19>
F:1579-1601/Product: genome-linked protein VPg1 #status predicted <VG1>

F:1602-1625/Product: genome-linked protein VPg2 #status predicted <VG2>
F:1626-1649/Product: genome-linked protein VPg3 #status predicted <VG3>

F:1650-1865/Product: proteinase #status predicted <PTS>
F:1663-2332/Product: RNA-directed RNA polymerase #status predicted <RRP>

Query Match 84.2% Score 85; DB 1; Length 2332;
Best Local Similarity 94.7% Pred. No. 4.7e-05;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGVRGDFGSLARVARQL 20
DB 864 GSGVRGDFGSLARVARQL 882

|||||
|||||

RESULT 2

A03911

genome polyprotein - foot-and-mouth disease virus A (strain A24 Cruzeiro) (fragment)

N:Contains: coat protein VP1; core protein p52
C:Species: Aphthovirus A (foot-and-mouth disease virus A)

C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 26-Aug-1999
C:Accession: A03911

R:Markoff, A.J.; Paynter, C.A.; Rowlands, D.J.; Boothroyd, J.C.
Nucleic Acids Res. 10, 8285-8295, 1982

A:Title: Comparison of the amino acid sequence of the major immunogen from three sero

A:Reference number: A37503; MUID:83143292; PMID:6298715
A:Accession: A03911
A:Molecule type: genomic RNA
A:Residues: 1-216 <MAK>
A:Cross-references: GB:J02183; NID:g210312; PIDN:AAA2596.1; PID:g210313
C:Comment: Specific enzymatic cleavage in vivo yields mature proteins including coat protein
C:Superfamily: foot-and-mouth disease virus genome polypeptide
C:Keywords: polypeptide

Query Match
Best Local Similarity 73.7%; Score 67; DB 2; Length 216;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 GSGVRGDFGSLARVAOL 20
Db 129 GSGVRGDFGSLARVAOL 147

RESULT 3
A03909
genome polypeptide - foot-and-mouth disease virus A (strain A5) (fragment)
N:Contains: coat protein VP1; coat protein VP3; coat protein VP2
C:Species: Aphthovirus A (foot-and-mouth disease virus A)
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 07-Feb-1997
C:Accession: A03909
R:Beck, E.; Feil, G.; Strohmater, K.
EMBO J. 2, 555-559, 1983
A:Title: The molecular basis of the antigenic variation of foot-and-mouth disease virus.
A:Reference number: A03909; MUID:84028562; PMID:6194987
A:Accession: A03909
A:Molecule type: mRNA
A:Residues: 1-230 <BEC>
A:Note: the authors translated the codon GCA for residue 114 as Val
C:Comment: Specific enzymatic cleavages in vivo yield mature proteins including the capsid
C:Superfamily: foot-and-mouth disease virus genome polypeptide
C:Keywords: polypeptide

Query Match
Best Local Similarity 57.9%; Score 50; DB 2; Length 230;
Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 2 GSGVRGDFGSLARVAOL 20
Db 143 GSGVRGDFGSLARVAOL 161

RESULT 4
S37077
genome polypeptide - foot-and-mouth disease virus A (strain A22/550 Azerbaijan 65)
N:Contains: coat protein VP1; coat protein VP2; coat protein VP3; coat protein VP4; coat protein VP2; genome-linked protein VPg; nonstructural protein p20a; proteinase (EC 3.4.21.1)
C:Species: Aphthovirus A (foot-and-mouth disease virus A)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C:Accession: S37077; JN0413
R:Sosnovtsev, S.V.; Onischenko, A.M.; Petrov, N.A.; Kalashnikova, T.I.; Mamaeva, N.V.; D
submitted to the EMBL Data Library, August 1993
A:Reference number: S37077
A:Accession: S37077
A:Molecule type: genomic RNA
A:Residues: 1-2336 <SOS>
A:Cross-references: EMBL:X4812; NID:g937965; PIDN:CAA52812.1; PID:g937966
R:Onischenko, A.M.; Petrov, N.A.; Bilinov, V.M.; Vassilenko, S.K.; Sandakchlev, L.S.; B
Bioorg. Khim. 12, 416-419, 1986
A:Title: The DNA-copy primary structure for the gene of the FMDV A22 serotype VP1-protein
A:Reference number: JN0413; MUID:86186952; PMID:2421736
A:Accession: JN0413
A:Molecule type: genomic RNA
A:Residues: 702-955 <ONI>
A:Cross-references: GB:M38362; NID:g210514; PIDN:AAA42664.1; PID:g210515
C:Superfamily: foot-and-mouth disease virus genome polypeptide
C:Keywords: coat protein; core protein; genome-linked protein; hydrolase; nonstructural
F:1-217/Product: nonstructural protein p20a #status predicted <NP4>
F:218-286/Product: coat protein VP4 #status predicted <VP4>

F:287-504/Product: coat protein VP2 #status predicted <VP2>
F:505-724/Product: coat protein VP3 #status predicted <VP3>
F:725-938/Product: coat protein VP1 #status predicted <VP1>
F:939-954/Product: core protein X #status predicted <CPX>
F:955-1108/Product: core protein p14 #status predicted <C14>
F:1109-1448/Product: core protein p14 #status predicted <C14>
F:1427-1579/Product: core protein p19 #status predicted <C19>
F:1580-1602/Product: genome-linked protein VPg1 #status predicted <VG1>
F:1603-1626/Product: genome-linked protein VPg2 #status predicted <VG2>
F:1627-1650/Product: genome-linked protein VPg3 #status predicted <VG3>
F:1651-1863/Product: proteinase #status predicted <PPS>
F:1864-2333/Product: RNA-directed RNA polymerase #status predicted <RRP>

Query Match
Best Local Similarity 63.2%; Score 50; DB 2; Length 2336;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 2 GSGVRGDFGSLARVAOL 20
Db 865 GSGVRGDFGSLARVAOL 883

RESULT 5
F90965
hypothetical protein EC52694 [imported] - Escherichia coli (strain O157:H7, substrain
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: F90965
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kohata, S.; Shiba, T.; Hattori, M.; Shimagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F90965
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-564 <HAY>
A:Cross-references: GB:BA00007; PIDN:BA836117.1; PID:g13362162; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: EC52694

Query Match
Best Local Similarity 47.5%; Score 48; DB 2; Length 564;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 4 GVRGDFGSLAL 14
Db 350 GVRGDFGSLAL 360

RESULT 6
F85813
hypothetical protein Z3047 [imported] - Escherichia coli (strain O157:H7, substrain E
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: F85813
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Linn, A.; Dimlanta, E.; Potamousts, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: AB5480; MUID:21074935; PMID:11206551
A:Accession: F85813
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-564 <STO>
A:Cross-references: GB:AE005174; NID:g12516062; PIDN:AA656970.1; GSPDB:GN00145; UNCP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z3047

Query Match
Best Local Similarity 47.5%; Score 48; DB 2; Length 564;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 4 GVRGDFGSLAL 14
|||||
Db 350 GVRGDFGSI 360

RESULT 7
H64959
probable membrane protein b1956 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: H64959
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: H64959
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-569 <BLAT>
A:Cross-references: GB:AE000287; GB:U00096; NID:g1788257; PIDN:AAC75022.1; PID:g1788266;
C:Genetics:
A:Start codon: TTG
C:Keywords: transmembrane protein
F:30-46/Domain: transmembrane #status predicted <TM1>
F:363-379/Domain: transmembrane #status predicted <TM2>

Query Match 47.5%; Score 48; DB 2; Length 569;
Best Local Similarity 72.7%; Pred. No. 10;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 4 GVRGDFGSLAL 14
|||||
Db 355 GVRGDFGSI 365

RESULT 8
GNNY2E
genome polypotein - foot-and-mouth disease virus A (strain A110161)
N:Contains: coat protein VP1; coat protein VP2; coat protein VP3; coat protein VP4; core
protein p20a; nonstructural protein p20b; RNA-directed RNA polymerase (EC 2.7.7.48)
C:Species: Aphthovirus A (foot-and-mouth disease virus A)
C:Date: 17-Dec-1982 #sequence_revision 28-Aug-1985 #text_change 16-Jul-1999
C:Accession: A93508; A91491; S30753
R:Carroll, A.R.; Rowlands, D.J.; Clarke, B.E.
Nucleic Acids Res. 12, 2461-2472, 1984
A:Title: The complete nucleotide sequence of the RNA coding for the primary translation
A:Reference number: A93508; MUID:84169547; PMID:6324120
A:Accession: A93508
A:Molecule type: genomic RNA
A:Residues: 1-2333 <CAR>
A:Cross-references: GB:X00429
R:Boothroyd, J.C.; Harris, T.J.R.; Rowlands, D.J.; Lowe, P.A.
Gene 17, 153-161, 1982
A:Title: The nucleotide sequence of cDNA coding for the structural proteins of foot-and-
A:Reference number: A91491; MUID:82211814; PMID:6282711
A:Accession: A91491
A:Molecule type: genomic RNA
A:Residues: 115-395, 'C', 397-631, 'U', 633-1048 <BOO>
A:Cross-references: GB:V01130; NID:961048; PIDN:CAA24361.1; PID:g1335402
R:Sanjar, D.V.; Newton, S.E.; Rowlands, D.J.; Clarke, B.E.
Nucleic Acids Res. 15, 3305-3315, 1987
A:Title: All foot and mouth disease virus serotypes initiate protein synthesis at two se
A:Reference number: S30753; MUID:87203363; PMID:3033601
A:Accession: S30753
A:Molecule type: genomic RNA
A:Residues: 1-32 <SAN>
A:Cross-references: EMBL:M31575; NID:g210486; PIDN:AAA42655.1; PID:g210487
C:Superfamily: foot-and-mouth disease virus genome polypotein
C:Keywords: coat protein; core protein; genome-linked protein; nonstructural protein; nu

F:1-204/Product: nonstructural protein p20a #status predicted <NPA>
F:205-286/Product: coat protein VP4 #status predicted <VP4>
F:287-504/Product: coat protein VP2 #status predicted <VP2>
F:505-725/Product: coat protein VP3 #status predicted <VP3>
F:726-937/Product: coat protein VP1 #status predicted <VP1>
F:938-1578/Product: core protein p52 #status predicted <CPP>
F:1579-1601/Product: genome-linked protein VPg1 #status predicted <GL1>
F:1602-1625/Product: genome-linked protein VPg2 #status predicted <GL2>
F:1626-1649/Product: genome-linked protein VPg3 #status predicted <GL3>
F:1650-1863/Product: nonstructural protein p20b #status predicted <NPB>
F:1864-2333/Product: RNA-directed RNA polymerase #status predicted <RRP>

Query Match 47.5%; Score 48; DB 1; Length 2333;
Best Local Similarity 71.4%; Pred. No. 1;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 7 GDFGSLARVAROL 20
|||||
Db 869 GDFGSLARVAROL 882

RESULT 9
T35564
ribosomal protein S9 - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 19-May-2000
C:Accession: T35564
R:Saunders, D.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1998
A:Reference number: 221583
A:Accession: T35564
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-170 <SAU>
A:Cross-references: EMBL:AL031317; PIDN:CAA20391.1; GSPDB:GN00070; SCOEDB:SC664.13
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: rpsL; SCOEDB:SC664.13
C:Superfamily: Escherichia coli ribosomal protein S9

Query Match 46.5%; Score 47; DB 2; Length 170;
Best Local Similarity 57.9%; Pred. No. 4;
Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 2 GSGVRGDFGSLARVAROL 20
|||||
Db 108 GSGVRGDFGSLARVAROL 126

RESULT 10
S61252
genome polypotein - foot-and-mouth disease virus Asia (isolate Asia I Mandya, Karnat
N:Alternate names: immunogenic polypotein
C:Species: Aphthovirus Asia (foot-and-mouth disease virus Asia)
A:Variety: isolate Asia I Mandya, Karnataka
C:Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 26-Aug-1999
C:Accession: S61252
R:Tulasiram, P.; Tyagi, M.; Suryanarayana, V.
submitted to the EMBL Data Library, June 1995
A:Description: Antigenic variation in foot and mouth disease virus type Asia I isolat
A:Reference number: S61252
A:Accession: S61252
A:Molecule type: mRNA
A:Residues: 1-109 <TUU>
A:Cross-references: EMBL:X88856; NID:g971407; PIDN:CAA61326.1; PID:g971408
A:Experimental source: isolate Asia I Mandya, Karnataka
C:Superfamily: foot-and-mouth disease virus genome polypotein
C:Keywords: coat protein; polypotein; proteinase
F:1-91/Product: coat protein VP1 (fragment) #status predicted <MAT1>
F:92-107/Product: proteinase 2A #status predicted <MAT2>
F:108-109/Product: proteinase 2B (fragment) #status predicted <MAT3>

Query Match 44.6%; Score 45; DB 2; Length 109;

C:Accession: S23355
R.Wu, F.M.; Wang, T.T.; Hsu, W.H.
FEMS Microbiol. Lett. 82, 313-318, 1991
A:Title: The nucleotide sequence of Schwannomyces occidentalis alpha-amylase gene.
A:Reference number: S23355
A:Accession: S23355
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-512 <WGF>
A:Cross-references: EMBL:X62079; NID:94880; PIDN:CAA43995.1; PID:94881
A:Note: the authors translated the codon AGA for residue 21 as Pro, CTT for residue 61 as
C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase
F:209-336/Domain: alpha-amylase core homology <AMY>

Query Match 43.6%; Score 44; DB 2; Length 512;
Best Local Similarity 47.1%; Pred. No. 40;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 CGSGVRGDFGSLALRA 17
| | ||||| : :
Db 475 CNSVSAGDFGSLYSIS 491

Search completed: October 9, 2003, 10:18:42
Job time : 21.6667 secs

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OM protein - protein search, using sw model

Run on: October 9, 2003, 10:02:54 ; Search time 10.3333 Seconds

(without alignments)
91.019 Million cell updates/sec

Title: US-09-549-186b-8

Perfect score: 101

Sequence: 1 CGSGVRGDFGSLARVARQL 20

Scoring table: BLOSUM62

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Length | ID | Description |
|------------|-------|-------|--------|----|-------------|
| 1 | 85 | 84.2 | 2332 | 1 | POLG_FMDVA |
| 2 | 67 | 66.3 | 216 | 1 | POLG_FMDVC |
| 3 | 50 | 49.5 | 230 | 1 | POLG_FMDVZ |
| 4 | 50 | 49.5 | 2336 | 1 | POLG_FMDVZ |
| 5 | 48 | 47.5 | 564 | 1 | YEDQ_ECO57 |
| 6 | 48 | 47.5 | 564 | 1 | YEDQ_ECO57 |
| 7 | 48 | 47.5 | 2333 | 1 | POLG_FMDV1 |
| 8 | 47 | 46.5 | 170 | 1 | RS9_FMDV1 |
| 9 | 45 | 44.6 | 110 | 1 | RS9_STRCO |
| 10 | 45 | 44.6 | 110 | 1 | INS_PSOAB |
| 11 | 44 | 43.6 | 348 | 1 | ADH1_PICST |
| 12 | 43.5 | 43.1 | 429 | 1 | YIZ9_CAEEL |
| 13 | 43 | 42.6 | 108 | 1 | HRB1_YEAST |
| 14 | 43 | 42.6 | 129 | 1 | INS1_MOUSE |
| 15 | 43 | 42.6 | 281 | 1 | RS9_CHLRE |
| 16 | 43 | 42.6 | 312 | 1 | EPID_HUMAN |
| 17 | 43 | 42.6 | 2205 | 1 | TRAD_HUMAN |
| 18 | 43 | 42.6 | 2207 | 1 | POLG_POL2M |
| 19 | 42 | 41.6 | 110 | 1 | POLG_POL2L |
| 20 | 42 | 41.6 | 173 | 1 | INS1_RAT |
| 21 | 42 | 41.6 | 173 | 1 | INS1_RAT |
| 22 | 42 | 41.6 | 309 | 1 | NU6M_SCYCA |
| 23 | 42 | 41.6 | 350 | 1 | FLIH_TREPA |
| 24 | 42 | 41.6 | 486 | 1 | ADH1_CANAL |
| 25 | 41.5 | 41.1 | 110 | 1 | KIC0_XENLA |
| 26 | 41 | 40.6 | 128 | 1 | INS2_RAT |
| 27 | 41 | 40.6 | 136 | 1 | RS9_CYACA |
| 28 | 41 | 40.6 | 348 | 1 | RS9_MYCPU |
| 29 | 41 | 40.6 | 351 | 1 | ADH2_PICST |
| 30 | 41 | 40.6 | 351 | 1 | NOV_RAT |
| 31 | 41 | 40.6 | 357 | 1 | REOA_TREPA |
| 32 | 41 | 40.6 | 759 | 1 | YMT1_YEAST |
| 33 | 41 | 40.6 | 5147 | 1 | CI02_MOUSE |
| | | | | | FAT_DROME |

| | | | | | | |
|----|------|------|-----|---|------------|---------------------|
| 34 | 40.5 | 40.1 | 555 | 1 | YKQC_BACSU | Q45493 bacillus su |
| 35 | 40.5 | 40.1 | 933 | 1 | PERT_CANFA | Q8HYB7 canis famil |
| 36 | 40 | 39.6 | 130 | 1 | RS9_XANCP | Q8PD41 xanthomonas |
| 37 | 40 | 39.6 | 130 | 1 | RS9_XANCP | Q8PD66 xanthomonas |
| 38 | 40 | 39.6 | 130 | 1 | RS9_XYLFRA | Q8PD43 xylella fas |
| 39 | 40 | 39.6 | 134 | 1 | RS9_THEMA | Q9X194 thermotoga |
| 40 | 40 | 39.6 | 151 | 1 | RS9_MYCPU | Q06259 mycobacteri |
| 41 | 40 | 39.6 | 153 | 1 | RS9_MYCPU | P40828 mycobacteri |
| 42 | 40 | 39.6 | 281 | 1 | WS22_MOUSE | Q9CY21 mus musculu |
| 43 | 40 | 39.6 | 311 | 1 | PUR2_MOUSE | P52421 vigna unguil |
| 44 | 40 | 39.6 | 347 | 1 | ADH1_YEAST | P00330 saccharomyc |
| 45 | 40 | 39.6 | 347 | 1 | ADH2_KLUMA | Q9P4C2 kluyveromyc |

ALIGNMENTS

RESULT 1
POLG_FMDVA STANDARD; PRT: 2332 AA.
AC P03308: P03312: Q65038: Q65039: Q65040: Q65041: Q65042: Q65043:
AD Q65044: Q65045: Q65046: Q65047:
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Genome polypeptide [Contains: Nonstructural protein P20A; Coat
proteins VP1 TO VP4; Core proteins X, P14, P41, P19; Genome-linked
DE proteins VP3 TO VP3; Picornain 3C (EC 3.4.22.28) (Protease 3C)
DE (P3C); RNA-directed RNA polymerase (EC 2.7.7.48)].
OS Foot-and-mouth disease virus (strain A12) (Aphthovirus A) (FMDV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_Taxid=12114;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=85211015; PubMed=2987518;
RX Roberton B.H., Grubman M.J., Weddell G.N., Moore D.M., Welsh J.D.,
RA Fischer T., Dowbenko D.J., Yansura D.G., Small B., Kield D.G.;
RT "Nucleotide and amino acid sequence coding for polypeptides of
RT foot-and-mouth disease virus type A12".
RL J. Virol. 54:651-660(1985).
[2]
RN SEQUENCE OF 1863-2332 FROM N.A.
RP MEDLINE=83225613; PubMed=6305004;
RX Roberton B.H., Morgan D.O., Moore D.M., Grubman M.J., Card J.,
RA Fischer T., Weddell G.N., Dowbenko D.J., Yansura D.G.;
RT "Identification of amino acid and nucleotide sequence of the
RT foot-and-mouth disease virus RNA polymerase".
RL Virology 126:614-623(1983).
[3]
RN SEQUENCE OF 715-955 FROM N.A.
RP MEDLINE=82061853; PubMed=6272395;
RX Kield D.G., Yansura D.G., Small B., Dowbenko D.J., Moore D.M.,
RA Grubman M.J., Kerecher P.D., Morgan D.O., Roberton B.H.,
RA Bachrach H.L.;
RT "Cloned viral protein vaccine for foot-and-mouth disease: responses
RT in cattle and swine".
RL Science 214:1125-1129(1981).
[4]
RN CATALYTIC ACTIVITY: Selective cleavage of Gln-1-gly bond in the
RN poliovirus polyprotein. In other picornavirus reactions Gln may be
RN substituted for Gln, and Ser or Thr for Gly.
[5]
RN CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
RN (RNA)(N).
[6]
RN SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS.
RN EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
RN VP3, AND VP4.
[7]
RN SPECIFIC ENZYMOLOGICAL CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
[8]
RN SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.

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DR EMBL: M10975; AAA42593.1; -
DR EMBL: J02187; AAA42670.1; -
DR MEROPS: C03.008; -
DR InterPro: IPR004004; Calic1_pol_hel.
DR InterPro: IPR004080; FMDVPlcoat.
DR InterPro: IPR001676; Rhv.
DR InterPro: IPR000605; RNA_helicase.
DR InterPro: IPR007095; RNA_pol_DS_PS.
DR InterPro: IPR001205; RNA_pol_P3D.
DR InterPro: IPR007094; RNA_pol_PSVlr.
DR Pfam: PF00073; rhv; 3.
DR Pfam: PF00680; RNA_dep_RNA_pol; 1.
DR Pfam: PF00910; RNA_helicase; 1.
DR PRINTS: PR00918; CALICIVIRUS.
DR PRINTS: PR01542; FMDVPlcoat.
KM Polypeptide; Coat protein; Core protein; RNA-directed RNA polymerase;
KM Transferase; Hydrolase; Thiol protease; Nonstructural protein;
KW Myristate.
FT CHAIN 1 200 NONSTRUCTURAL PROTEIN P20A.
FT CHAIN 201 285 COAT PROTEIN VP4.
FT CHAIN 286 503 COAT PROTEIN VP2.
FT CHAIN 504 723 COAT PROTEIN VP3.
FT CHAIN 724 937 COAT PROTEIN VP1.
FT CHAIN 938 953 CORE PROTEIN X.
FT CHAIN 954 1107 CORE PROTEIN P14.
FT CHAIN 1108 1425 CORE PROTEIN P19.
FT CHAIN 1426 1578 CORE PROTEIN P41.
FT CHAIN 1579 1601 GENOME-LINKED PROTEIN VP1.
FT CHAIN 1602 1625 GENOME-LINKED PROTEIN VP2.
FT CHAIN 1626 1649 GENOME-LINKED PROTEIN VP3.
FT CHAIN 1650 1862 PROTEASE.
FT CHAIN 1863 2332 RNA-DIRECTED RNA POLYMERASE.
FT LIPID 201 MYRISTATE.
SQ SEQUENCE 2332 AA; 259408 MW; EE77DA739CBEC6A CRC64;

Query Match 84.2%; Score 85; DB 1; Length 2332;
Best Local Similarity 94.7%; Pred. No. 2.3e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 GSGRGDFGSLARVAROL 20
DB 864 GSGRGDFGSLARVAROL 882

RESULT 2
POLG_FMDVC STANDARD; PRT; 216 AA.
AC P03309;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Genome polypeptide [contains: Coat protein VP1; Core protein P52]
DE (Fragment).
OS Foot-and-mouth disease virus (strain A24 Cruzeiro) (Aphthovirus A)
OS (FMDV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
NCBI_Taxid=12115;
RN NCHI [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83143292; PubMed=6298715;
RA Makoff A.J., Paynter C.A., Rowlands D.J., Boothroyd J.C.;
RT "Comparison of the amino acid sequence of the major immunogen from
RT three serotypes of foot and mouth disease virus.";
RL Nucleic Acids Res. 10:8285-8295(1982).
-1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC VP3 AND VP4.
-1- PFM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.

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DR EMBL: J02183; AAA42596.1; -
DR EMBL: A06733; CAA00589.1; -
DR PIR: A03911; A03911.
DR HSSP: Q88571; 1TME.
DR InterPro: IPR004080; FMDVPlcoat.
DR InterPro: IPR001676; Rhv.
DR Pfam: PF00073; rhv; 1.
DR PRINTS: PR01542; FMDVPlcoat.
KM Coat protein; Core protein; Polypeptide.
FT NON_TER 1 1
FT CHAIN 1 202 COAT PROTEIN VP1.
FT CHAIN 203 >216 CORE PROTEIN P52.
FT NON_TER 216 216
SQ SEQUENCE 216 AA; 23889 MW; 501659FF031A1D85 CRC64;

Query Match 66.3%; Score 67; DB 1; Length 216;
Best Local Similarity 73.7%; Pred. No. 0.0015;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 GSGRGDFGSLARVAROL 20
DB 129 GSGRGDFGSLARVAROL 147

RESULT 3
POLG_FMDVS STANDARD; PRT; 230 AA.
AC P03307;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Genome polypeptide [contains: Coat proteins VP3, VP1; Core protein
DE P52] (Fragment).
OS Foot-and-mouth disease virus (strain A5) (Aphthovirus A) (FMDV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
NCBI_Taxid=12113;
RN NCHI [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84028562; PubMed=6194987;
RA Beck E., Fell G., Strohmaier K.;
RT "The molecular basis of the antigenic variation of foot-and-mouth
RT disease virus.";
RL EMBO J. 2:555-559(1983).
-1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC VP3 AND VP4.
-1- PFM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
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DR EMBL: V01135; CAA24365.1; ALT_INIT.
DR EMBL: V01135; CAA24366.1; ALT_SEQ.
DR PIR: A03909; A03909.
DR HSSP: Q88571; 1TME.
DR InterPro: IPR004080; FMDVPlcoat.
DR InterPro: IPR001676; Rhv.
DR Pfam: PF00073; rhv; 1.

DR PRINTS; PR01542; FMDVICOAT.
DR CoAT protein; Core protein; Polypeptide.
KW NON_TER 1 1
FT CHAIN <1 4 COAT PROTEIN VP3.
FT CHAIN 5 216 COAT PROTEIN VP1.
FT CHAIN 217 >230 CORE PROTEIN P52.
FT NON_TER 230 230
SQ SEQUENCE 230 AA; EA93A190F4CC1608 CRC64;
Query Match 49.5%; Score 50; DB 1; Length 230;
Best Local Similarity 57.9%; Pred. No. 0.86;
Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
OY 2 GSGVGDGSLARVROL 20
DB 143 GPRRGDMSAARAQOL 161
RESULT 4
POLG_FMDVZ STANDARD; PRT; 2336 AA.
ID AC P49303;
DT 01-FEB-1996 (Rel. 33, Last Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Genome polypeptide [contains: Nonstructural protein P20A; CoAT
proteins VP1 TO VP4; Core proteins X, P14, P41, P19; Genome-linked
proteins VP3 TO VP3; Picornain 3C (EC 3.4.22.28) (Protease 3C)
P1C]; RNA-directed RNA polymerase (EC 2.7.7.48)].
OS Foot-and-mouth disease virus (Strain A22/550 Azerbaijan 65)
OC (Aphthovirus A) (FMDV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=73481;
RN [1]
RP SEQUENCE FROM N.A.
RA Sosnovsev S.V., Onischenko A.M., Petrov N.A., Kalashnikova T.I.,
Manueva N.V., Drygin V.Y., Perevozchikova N.A., Vasilenko S.K.;
Submitted (Aug-1993) to the EMBL/GenBank/DBJ databases.
RL CATALYTIC ACTIVITY: Selective cleavage of Glu-1-Gly bond in the
poliovirus polypeptide. In other picornavirus reactions Glu may be
substituted for Gln, and Ser or Thr for Gly.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
(RNA)(N).
CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAEDRAL UNITS,
EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
VP3, AND VP4.
CC -1- PFM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
CC -----
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or send an email to license@sib-sib.ch).
CC -----
DR EMBL; X74812; CA552812.1; -
DR PIR; S37077; S37077.
DR HSSP; Q88571; ITME.
DR MEROPS; C03.008; -
DR MEROPS; C28.001; -
DR InterPro: IPR004004; Calic1_pol_hel.
DR InterPro: IPR004080; FMDVICOAT.
DR InterPro: IPR001676; RNV.
DR InterPro: IPR000605; RNA_helicase.
DR InterPro: IPR007095; RNA_pol_DS_PS.
DR InterPro: IPR001205; RNA_pol_P3D.
DR InterPro: IPR007094; RNA_pol_PSVir.
DR Pfam; PF00073; rhv, 3.
DR Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR Pfam; PF00910; RNA_helicase; 1.

DR PRINTS; PR00918; CALICVIRUSNS.
DR PRINTS; PR01542; FMDVICOAT.
DR Polypeptide; CoAT protein; Core protein; RNA-directed RNA polymerase;
KW Transferase; Hydrolase; Thiol protease; Nonstructural protein;
KW Myristate.
FT CHAIN 1 201 NONSTRUCTURAL PROTEIN P20A.
FT CHAIN 202 286 COAT PROTEIN VP4.
FT CHAIN 287 504 COAT PROTEIN VP2.
FT CHAIN 505 724 COAT PROTEIN VP3.
FT CHAIN 725 938 COAT PROTEIN VP1.
FT CHAIN 939 954 CORE PROTEIN X.
FT CHAIN 955 1108 CORE PROTEIN P14.
FT CHAIN 1109 1426 CORE PROTEIN P19.
FT CHAIN 1427 1579 CORE PROTEIN P41.
FT CHAIN 1580 1602 GENOME-LINKED PROTEIN VP3.
FT CHAIN 1603 1626 GENOME-LINKED PROTEIN VP2.
FT CHAIN 1627 1650 GENOME-LINKED PROTEIN VP3.
FT CHAIN 1651 1863 PROTEASE.
FT CHAIN 1864 2336 RNA-DIRECTED RNA POLYMERASE.
FT LIPID 202 202 MYRISTATE (BY SIMILARITY).
SQ SEQUENCE 2336 AA; 259982 MW; 15AC2AB022B5B954 CRC64;
Query Match 49.5%; Score 50; DB 1; Length 2336;
Best Local Similarity 63.2%; Pred. No. 9.5;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
OY 2 GSGVGDGSLARVROL 20
DB 865 GMRGRDLEPLARVROL 883
RESULT 5
YEDQ_ECO57 STANDARD; PRT; 564 AA.
ID AC Q8XB92;
DT 28-FEB-2003 (Rel. 41, Last Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein yedQ.
GN YEDQ OR Z3047 OR EC52694.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-O157:H7 / EDU933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perina N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouls K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blatter F.R.;
RA "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RT Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori K., Shinagawa C., Higashigawa T.,
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12";
RL DNA Res. 8:11-22(2001).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE YAC / YFIN (E.COLI), YHCK (B.SUBTILIS)
CC FAMILY.
CC -1- SIMILARITY: Contains 1 GDEF domain.
CC -----
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DR EMBL; AE005417; AAG56970.1; -
DR EMBL; AP002559; BAB36117.1; -
DR PIR; F90965; F90965.
DR InterPro; IPR000160; GGDEF.
DR Pfam; PF00990; GGDEF. 1.
DR SMART; SM00267; DUF1. 1.
DR TIGRFAMs; TIGR00254; GGDEF. 1.
DR PROSITE; PS00887; GGDEF. 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 20 40 POTENTIAL.
FT TRANSMEM 360 380 POTENTIAL.
FT DOMAIN 428 563 GGDEF.
SQ SEQUENCE 564 AA; 64287 MW; BEBC2286ADBAECB0 CRC64;

Query Match 47.5%; Score 48; DB 1; Length 564;
Best Local Similarity 72.7%; Pred. No. 4.6;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 4 GVRGDFGSLAL 14
DB 350 GVRGDFGSLIST 360

RESULT 6
YEDO_ECOLI STANDARD: PRT; 564 AA.
AC P76330; P94746;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein yedQ.
GN YEDO OR B1956.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655.
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kaeai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA Mizobuchi K., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y.,
RA Sivasubram S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horinouchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE YAC / YFIN (E.COLI), YHCK (B.SUBTILIS)
CC FAMILY.
CC -1- SIMILARITY: Contains 1 GGDEF domain.
CC -----
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DR EMBL; AE000287; AAC75022.1; ALT_INIT.
DR EMBL; D90835; BAA15784.1; -
DR Ecogene; EG14040; yedQ.
DR InterPro; IPR000160; GGDEF.
DR Pfam; PF00990; GGDEF. 1.
DR SMART; SM00267; DUF1. 1.
DR TIGRFAMs; TIGR00254; GGDEF. 1.
DR PROSITE; PS00887; GGDEF. 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 20 40 POTENTIAL.
FT TRANSMEM 360 380 POTENTIAL.
FT DOMAIN 428 563 GGDEF.
SQ SEQUENCE 564 AA; 64283 MW; 05FB02C1BE2A8938 CRC64;

Query Match 47.5%; Score 48; DB 1; Length 564;
Best Local Similarity 72.7%; Pred. No. 4.6;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 4 GVRGDFGSLAL 14
DB 350 GVRGDFGSLIST 360

RESULT 7
POLG_FMDV1 STANDARD: PRT; 2333 AA.
AC P03306; Q64768; Q84750; Q84751; Q84752; Q84753; Q84754; Q84760;
AC Q84761; Q84762; Q84763; Q84764; Q84765; Q84766; Q84767; Q84768;
AC Q84769; Q89824;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Genome polyprotein [Contains: Nonstructural protein p20a; Coat
DE proteins VP1 TO VP4; Core protein p52; Genome-linked proteins VPg1 TO
DE VPg3; Picornain 3C (EC 3.4.22.28) (Protease 3C) (P3C); RNA-directed
DE RNA polymerase p56a (EC 2.7.7.48)].
OS Foot-and-mouth disease virus (strain A10-61) (Aphthovirus A) (FMDV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12112;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=84169547; PubMed=6324120;
RA Carroll A.R., Rowlands D.J., Clarke B.E.;
RT "The complete nucleotide sequence of the RNA coding for the primary
RT translation product of foot and mouth disease virus.";
RL Nucleic Acids Res. 12:2461-2472(1984).
RN [2]
RP SEQUENCE OF 115-1048 FROM N.A.
RX MEDLINE=82211814; PubMed=6282711;
RA Bocthoroy J.C., Harris T.J.R., Rowlands D.J., Lowe P.A.;
RT "The nucleotide sequence of cDNA coding for the structural proteins
RT of foot-and-mouth disease virus.";
RL Gene 17:153-161(1982).
CC -1- CATALYTIC ACTIVITY: Selective cleavage of Gln-|-Gly bond in the
CC poliovirus polypeptide. In other picornavirus reactions Gln may be
CC substituted for Gln, and Ser or Thr for Gly.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate -> N diphosphate +
CC (RNA)(N).
CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHERAL UNITS,
CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC VP3, AND VP4.
CC -1- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
CC -----
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CC -----

DR EMBL, V01130; CAA24361.1; -
 DR EMBL, X00429; CAA25127.1; -
 DR MEROPS; C03.008; -
 DR InterPro: IPR004004; Calicli_pol_hel.
 DR InterPro: IPR004080; FMDVp1coat.
 DR InterPro: IPR001676; Rny.
 DR InterPro: IPR006055; RNA_helicase.
 DR InterPro: IPR007095; RNA_pol_DS_Ps.
 DR InterPro: IPR001205; RNA_pol_P3D.
 DR InterPro: IPR007094; RNA_pol_PSVLr.
 DR Pfam; PF000073; rny; 3.
 DR Pfam; PF00680; RNA_dep_RNA_pol; 1.
 DR Pfam; PF00910; RNA_helicase; 1.
 DR PRINTS; PR00918; CALICVIRUSNS.
 DR PRINTS; PR01542; FMDVPLCOAT.
 DR Polypeptide; Coat protein; Core protein; RNA-directed RNA polymerase;
 DR Transferase; Hydrolase; Thiol protease; Nonstructural protein;
 DR Myristate.

ET CHAIN 1 201 NONSTRUCTURAL PROTEIN P20A.
 ET CHAIN 202 286 COAT PROTEIN VP4.
 ET CHAIN 287 504 COAT PROTEIN VP2.
 ET CHAIN 505 725 COAT PROTEIN VP3.
 ET CHAIN 726 937 COAT PROTEIN VP1.
 ET CHAIN 938 1578 CORE PROTEIN P52.
 ET CHAIN 1579 1601 GENOME-LINKED PROTEIN VP1.
 ET CHAIN 1602 1625 GENOME-LINKED PROTEIN VP2.
 ET CHAIN 1626 1649 GENOME-LINKED PROTEIN VP3.
 ET CHAIN 1650 1863 PROTEASE P20B.
 ET CHAIN 1864 2333 RNA-DIRECTED RNA POLYMERASE P56A.
 ET LIPID 202 302 MYRISTATE.
 ET CONFLICT 396 396 S -> C (IN REF. 2).
 ET CONFLICT 632 632 P -> L (IN REF. 2).
 ET SEQUENCE 2333 AA; 259645 MW; 4FC667DCC521B660 CRC64;

Query Match 47.5%; Score 48; DB 1; Length 2333;
 Best Local Similarity 71.4%; Pred. No. 20;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 7 GDFGSLARVAROL 20
 |||:| ||| |
 DB 869 GDLSIARVAROL 882

RESULT 8
 RS9_STRCO STANDARD; PRT; 170 AA.
 AC 053875;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 30S ribosomal protein S9.
 GN RPS1 OR SC04735 OR SC664.13.
 OS Streptomyces coelicolor.
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 CC Streptomycineae; Streptomycetaceae; Streptomyces.
 OC NCBI_TaxID=1902;
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=98102746; PubMed=9439573;
 RA Sanchez C., Bianco G., Mendez C., Salas J.A.;
 RT "Cloning, sequencing and transcriptional analysis of a Streptomyces
 RT ribosomal protein containing the rplM and rpsI genes encoding
 RT Mol. Gen. Genet. 257:91-96(1997).
 RL [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajadream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 CC -1- SIMILARITY: BELONGS TO THE S9P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----

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CC -----

DR EMBL, U43429; AAC46061.1; -
 DR EMBL, AL939121; CAA20391.1; -
 DR PIR; T35564; T35564.
 DR HAMAP; MF_00532; -; 1.
 DR InterPro: IPR00754; Ribosomal_S9.
 DR Pfam; PF00380; Ribosomal_S9; 1.
 DR ProDom; PD001627; Ribosomal_S9; 1.
 DR PROSITE; PS00360; RIBOSOMAL_S9; 1.
 DR Ribosomal protein; Complete proteome.
 KW Ribosomal protein; Complete proteome.
 SO SEQUENCE 170 AA; 18699 MW; 3CEE00FE69151C99 CRC64;

Query Match 46.5%; Score 47; DB 1; Length 170;
 Best Local Similarity 57.9%; Pred. No. 1.9;
 Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 2 GSGVRGDFGSLARVAROL 20
 |||:| ||| |
 DB 108 GGGVSGAGALRLGVARAL 126

RESULT 9
 INS_PSAOB STANDARD; PRT; 110 AA.
 AC 062587;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Insulin precursor.
 GN INS.
 OS Psammomyces obesus.
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
 CC Psammomyces.
 OC NCBI_TaxID=48139;
 OX NCBI_TaxID=48139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=97309250; PubMed=9166665;
 RA Kaiser N., Baillyes E.M., Schneider B.S., Cerasi E., Steiner D.F.,
 RA Hutton J.C., Gross D.J.;
 RT "Characterization of the unusual insulin of Psammomyces obesus, a
 RT rodent with nutrition-induced NIDDM-like syndrome.";
 RL Diabetes 46:953-957(1997).
 CC -1- FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT
 CC INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND
 CC FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE
 CC CYCLE, AND GLUCOGEN SYNTHESIS IN LIVER.
 CC -1- SUBUNIT: HETERODIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO

```
CC DISULFIDE BONDS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
CC -----
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CC -----
CC EMBL: X98241; CAA66897.1; -.
CC DR HSSP: P01308; 1A10.
CC DR InterPro: IPR004825; Ins/IGF/relax.
CC DR Pfam: PF00049; Insulin; 1.
CC DR PRINTS: PR00277; INSULINB.
CC DR SMART: SM00078; IIGF; 1.
CC DR PROSITE: PS00262; INSULIN; 1.
CC KW Insulin family; Hormone; Glucose metabolism; Signal.
CC FT SIGNAL 1 24
CC FT CHAIN 25 54
CC FT PROPEP 57 87
CC FT CHAIN 90 110
CC FT DISULFID 31 96
CC FT DISULFID 43 109
CC FT DISULFID 95 100
CC FT SEQUENCE 110 AA; 12324 MW; A006738E20579CB0 CRC64;
CC -----
Query Match 44.6%; Score 45; DB 1; Length 110;
Best Local Similarity 61.1%; Pred. No. 2.5;
Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 2 GSGVGRDGSGLALVARQ 19
Db 11 11 1111111
70 GSPGAGDLRALALEVARQ 87
CC -----
RESULT 10
ADH1_PICST STANDARD; PRT; 348 AA.
AC 000097;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alcohol dehydrogenase I (EC 1.1.1.1) (ADH 2).
GN ADH1 OR ADH2.
OS Pichia stipitis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4924;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 58785 / CBS 6054;
RX MEDLINE=98207839; PubMed=9546172;
RA Cho J.Y., Jeffries T.W.;
RT "Pichia stipitis genes for alcohol dehydrogenase with fermentative
RT and respiratory functions."
RL Appl. Environ. Microbiol. 64:1350-1358(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS 5774;
RX MEDLINE=99019018; PubMed=9802210;
RA Passoth V., Schaefer B., Liebel B., Weierstall T., Klinger U.;
RT "Molecular cloning of alcohol dehydrogenase genes of the yeast Pichia
RT stipitis and identification of the fermentative ADH.";
RL Yeast 14:1311-1325(1998)
CC -----
-1- FUNCTION: CONVERTS ETHANOL TO ACETALDEHYDE AND PLAYS A MAJOR ROLE
CC IN XYLISE FERMENTATION.
CC -1- CATALYTIC ACTIVITY: An alcohol + NAD(+) - an aldehyde or ketone +
CC NADH.
CC -1- COFACTOR: Binds 2 zinc ions per subunit (By similarity).
CC -1- SUBUNIT: Homotetramer (By similarity).
```

```
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
CC family.
CC -----
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CC -----
CC EMBL: AF008245; AAC49991.1; -.
CC DR EMBL: Y13397; CAA73827.1; -.
CC DR InterPro: IPR002328; ADH_zinc.
CC DR InterPro: IPR002085; Adh_zn family.
CC DR Pfam: PF00107; ADH_zinc_N; 1.
CC DR PROSITE: PS00059; ADH_ZINC; 1.
CC KW Oxidoreductase; Zinc; Metal-binding; NAD; Multigene family.
CC FT METAL 44 44
CC FT METAL 67 67
CC FT METAL 98 98
CC FT METAL 101 101
CC FT METAL 104 104
CC FT METAL 112 112
CC FT METAL 134 134
CC FT SEQUENCE 348 AA; 36520 MW; 49C06B545D5350P4 CRC64;
CC -----
Query Match 44.6%; Score 45; DB 1; Length 348;
Best Local Similarity 45.0%; Pred. No. 8.4;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY 1 CGSGVGRDGSGLALVARQ 20
Db 11 11 1111111
175 CISGAGGIGSLAIQYAKM 194
CC -----
RESULT 11
YLZ9_CAEEL STANDARD; PRT; 309 AA.
AC P34414;
DT 01-FEB-1994 (Rel. 28, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein F42H10.9 in chromosome III.
GN F42H10.9/F42H10.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
RA Sims M., Smaildon N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterson R., Watson A., Welstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
RN [2]
RP REVISIONS.
RA Waterson R.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
```


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DR EMBL; L08403; AAA28019.2; -
DR Wormpep; F42H10.9; CE24970.
KW Hypothetical protein.
SQ SEQUENCE 305 AA; 35071 MW; E2D47102CEB52B0A CRC64;

Query Match 43.6%; Score 44; DB 1; Length 309;
Best Local Similarity 64.7%; Pred. NO. 11;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 GSGVGDGSLALRYAR 18
DB 134 GDVVGAGGFWALRYAR 150

RESULT 12

ID HRB1_YEAST STANDARD; PRT; 429 AA.

AC P38922;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE HRB1 protein (TOM34 protein).

GN HRB1 OR TOM34 OR YNL004W OR N2009.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI_TaxID=4932;

RN [1]

SEQUENCE FROM N.A.

RC STRAIN=GRF88;

RA MEDLINE=94005822; PubMed=8402262;

RT Lalo D., Stettler S., Mariotte S., Slonimski P., Thuriaux P.;

RT "Two yeast chromosomes are related by a fossil duplication of their

RT centromeric regions.";

RT C. R. Acad. Sci., III, Sci. Vie 316:367-373(1993).

RL [2]

SEQUENCE FROM N.A.

RC STRAIN=GRF88;

RA MEDLINE=95028151; PubMed=7941739;

RT Lalo D., Stettler S., Mariotte S., Gendreau E., Thuriaux P.;

RT "Organization of the centromeric region of chromosome XIV in

RT Saccharomyces cerevisiae.";

RT Yeast 10:523-533(1994).

RL [3]

SEQUENCE FROM N.A.

RC STRAIN=S288C / FY1679;

RA MEDLINE=95076713; PubMed=7985421;

RT Vermaaselt P., Aert R., Voet M., Volckaert G.;

RT "Nucleotide sequence analysis of an 887 bp region of the left arm of

RT yeast chromosome XIV, encompassing the centromere sequence.";

RL Yeast 10:945-951(1994).

RL [1]

SUBCELLULAR LOCATION: Nuclear (Potential).

CC [1]

SIMILARITY: STRONG, TO YEAST GBP2.

CC [1]

SIMILARITY: Contains 3 RNA recognition motif (RRM) domains.

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DR EMBL; U02536; AAA64803.1; -

DR EMBL; X77114; CAA54378.1; -

DR EMBL; Z71280; CAA95863.1; -

DR PIR; S45459; S45459.

DR HSSP; P09651; IHA1.

DR SGD; S0004949; HRB1.

DR GO; GO:0005737; C:cytoplasm; IDA.

DR GO; GO:0030530; C:heterogeneous nuclear ribonucleoprotein com. .; NAS.

DR GO; GO:0006606; P:protein nucleus import; IPI.

DR Interpro; IPR000504; RNA_rec_mot.

DR Pfam; PF00076; rrm; 3.

DR SMART; SM00360; RRM; 3.

DR PROSITE; PS50102; RRM; 3.

DR PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.

DR RNA-binding; Nuclear protein; Repeat.

FT DOMAIN 136 212 RNA-BINDING (RRM) 1.

FT DOMAIN 236 313 RNA-BINDING (RRM) 2.

FT DOMAIN 351 428 RNA-BINDING (RRM) 3.

SQ SEQUENCE 429 AA; 49141 MW; DC0F732EFA43EEB9 CRC64;

Query Match 43.1%; Score 43.5; DB 1; Length 429;
Best Local Similarity 55.6%; Pred. NO. 18;
Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

OY 3 SGVGDGSLALRYARQL 20
DB 108 SGARDYGPL---LAREL 122

RESULT 13

ID INSL_MOUSE STANDARD; PRT; 108 AA.

AC P01325; Q9D907;

DT 21-JUL-1986 (Rel. 01, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Insulin 1 precursor.

GN INSL OR INS-1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

SEQUENCE FROM N.A.

RC MEDLINE=87169768; PubMed=3104603;

RA Wentworth B.M., Schaefer I.M., Villa-Komaroff L., Chirgwin J.M.;

RT "Characterization of the two nonallelic genes encoding mouse

RT preproinsulin.";

RT J. Mol. Evol. 23:305-312(1986).

RL [2]

SEQUENCE FROM N.A.

RC STRAIN=NON;

RA MEDLINE=90372989; PubMed=2397023;

RT Sawa T., Ohgaku S., Morioka H., Yano S.;

RT "Molecular cloning and DNA sequence analysis of preproinsulin genes

RT in the NON mouse, an animal model of human non-obese, non-insulin-

RT dependent diabetes mellitus.";

RT J. Mol. Endocrinol. 5:61-67(1990).

RL [3]

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Pancreas;

RA MEDLINE=21085660; PubMed=11217851;

RT Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.;

RT Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.;

RT Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.;

RT Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.;

RT Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.;

RT Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.;

RT Kuehl P., Lewis S., Matsuo Y., Mikalido I., Pesole G., Quackenbush J.;

RT Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.;

RT Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.;

RT Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.;

RT Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.;

RT Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.;

RT Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.;

RT Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.;

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:665-660(2001).
 RN
 RP SEQUENCE OF 25-54 AND 88-108.
 RX MEDLINE-72189455; PubMed-5063718;
 RA Buehler H.F., Glatthar B., Kunz P., Muehlhaupt E., Hummel R.E.;
 RT "Amino acid sequence of the two insulins from mouse (Maus musculus).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:451-458(1972).
 CC
 CC -1- FUNCTION: INSULIN DECREASES BLOOD GLUCOSE CONCENTRATION. IT
 CC INCREASES CELL PERMEABILITY TO MONOSACCHARIDES, AMINO ACIDS AND
 CC FATTY ACIDS. IT ACCELERATES GLYCOLYSIS, THE PENTOSE PHOSPHATE
 CC CYCLE, AND GLYCOGEN SYNTHESIS IN LIVER.
 CC
 CC -1- SUBUNIT: HETEROIDIMER OF A B CHAIN AND AN A CHAIN LINKED BY TWO
 CC SULFIDE BONDS.
 CC
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC
 CC -1- SIMILARITY: BELONGS TO THE INSULIN/IGF/RELAXIN FAMILY.
 CC
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 CC
 CC EMBL: X04725; CAA28634.1; -
 DR EMBL: AK007482; BAB25058.1; -
 DR PIR: B26342; INMSI.
 DR HSSP: P01308; IAF.
 DR MGD: MGI:96572; InsI.
 DR InterPro: IPR004825; Ins/IGF/relax.
 DR Pfam: PF000049; Insulin; 1.
 DR SMART: SM00078; IIGF; 1.
 DR PROSITE: PS00262; INSULIN; 1.
 DR Insulin family; Hormone; Glucose metabolism; Signal; Multigene family.
 KW SIGNAL
 FT CHAIN 1 24
 FT PROPEP 25 54 INSULIN 1 B CHAIN.
 FT CHAIN 57 85 INSULIN 1 C PEPTIDE.
 FT CHAIN 88 108 INSULIN 1 A CHAIN.
 FT DISULFID 31 94 INTERCHAIN.
 FT DISULFID 43 107 INTERCHAIN.
 FT DISULFID 93 98
 FT COMFLICT 37 37 E -> K (IN REF. 3).
 SQ SEQUENCE 108 AA; 12160 MW; F63D9B7B8960F88 CRC64;
 Query Match 42.6%; Score 43; DB 1; Length 108;
 Best Local Similarity 62.5%; Pred. No. 5.2;
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 Oy 4 GVRGDFGSLAVRQ 19
 Db 70 GSPDQLQTALEVARQ 85
 ID RS9_CHLITE STANDARD; PRT; 129 AA.
 AC Q8KBA5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 30S ribosomal protein S9.
 GN RPSI OR CT1782.
 OS Chlorobium leptidum.
 OC Bacteria; Chlorobi; Chlorobiales; Chlorobiaceae;
 OC Chlorobium.
 RT
 RX NCBI_TaxID=1097;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-TLS / ATCC 49652 / DSM 12025;
 RX MEDLINE-22103685; PubMed-12093901;
 RA Eiden J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
 RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
 RA Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parks D.,
 RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
 RA Vamathevan J., Khouli H., White O., Gruber T.M., Ketchum K.A.,
 RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
 RT "The complete genome sequence of Chlorobium leptidum TLS, a
 RT photosynthetic, anaerobic, green-sulfur bacterium.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
 CC
 CC -1- SIMILARITY: BELONGS TO THE S9P FAMILY OF RIBOSOMAL PROTEINS.
 CC
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 CC
 CC EMBL: AE012931; AAM73003.1; -
 DR TIGR: CT1782; -
 DR HAMAP: MF_00532; -; 1.
 DR InterPro: IPR000754; Ribosomal_S9.
 DR Pfam: PF00380; Ribosomal_S9; 1.
 DR ProDom: PD001627; Ribosomal_S9; 1.
 DR PROSITE: PS00360; RIBOSOMAL_S9; 1.
 KW Ribosomal protein; Complete proteome.
 SQ SEQUENCE 129 AA; 14541 MW; D110858BA87B9BAC CRC64;
 Query Match 42.6%; Score 43; DB 1; Length 129;
 Best Local Similarity 42.1%; Pred. No. 6.3;
 Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 Oy 2 GSGVRGDFGSLAVRQ 20
 Db 68 GCGILTGSGAVSLARAL 86
 ID EF1D_HUMAN STANDARD; PRT; 281 AA.
 AC P29692; Q969J1;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Elongation factor 1-delta (EF-1-delta) (Antigen NY-CO-4).
 GN Elongation factor 1-delta.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE-Skin fibroblast;
 RC MEDLINE-93326642; PubMed-8334168;
 RX Sanders J.P., Raggiasschi R., Morales J., Moeller W.;
 RT "The human leucine zipper-containing guanine-nucleotide exchange
 RT protein elongation factor-1 delta.";
 RL Biochim. Biophys. Acta 1174:87-90(1993).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE-Colorectal carcinoma;
 RC MEDLINE-98272252; PubMed-9610721;
 RX Scanlan M.J., Chen Y.-T., Williamson B., Gure A.O., Stockert E.,
 RA Gordon J.D., Tureci O., Sahin U., Pfeundschn M., Old L.J.;
 RT "Characterization of human colon cancer antigens recognized by
 RT autologous antibodies.";
 RL Int. J. Cancer 76:652-658(1998).
 RN [3]

```

RP  SEQUENCE FROM N.A.
RC  TISSUE-Muscle;
RX  MEDLINE=22388257; PubMed=12477932;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA  Baha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA  Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Wotley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA  Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA  Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA  Schnerch A., Schein J.E., Jones S.J.M., Maira M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length
RT  human and mouse cDNA sequences."
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC  -1- FUNCTION: EF-1-BETA AND EF-1-DELTA STIMULATE THE EXCHANGE OF
CC  GDP BOUND TO EF-1 ALPHA TO GTP.
CC  -1- SUBUNIT: EF-1 IS COMPOSED OF FOUR SUBUNITS: ALPHA, BETA,
CC  DELTA, AND GAMMA.
CC  -1- SIMILARITY: BELONGS TO THE EF-1-BETA/EF-1-DELTA FAMILY.
CC  -----
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CC  -----
DR  EMBL; Z21507; CAA79716.1; -.
DR  EMBL; BC008012; AAH08012.1; -.
DR  EMBL; BC009907; AAH09907.1; -.
DR  EMBL; BC012819; AAH12819.1; -.
DR  PIR; S34626; S34626.
DR  Genew; HGNC:3211; EEF1D.
DR  MIM; 130592; -.
DR  GO; GO:0005853; C:eukaryotic translation elongation factor 1 . . . ; TAS.
DR  InterPro; IPR001326; EF1_BD.
DR  Pfam; PF00736; EF1BD; 1.
DR  PROSITE; PS00824; EF1BD_1; 1.
DR  PROSITE; PS00825; EF1BD_2; 1.
DR  PROSITE; PS00825; EF1BD_2; 1.
DR  Elongation factor; Protein biosynthesis.
KW  CONFLICT 34 34 A -> R (IN REF. 1).
FT  CONFLICT 44 44 S -> T (IN REF. 1).
SQ  SEQUENCE 281 AA; 31122 MW; CE78BD6D5D09BD6C CRC64;

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Query Match 42.6%; Score 43; DB 1; Length 281;
Best Local Similarity 53.3%; Pred. NO. 14;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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Oy 3 SGVRGDFGSLARVA 17
    || || | | | : | : |
Db 71 SGTSGDHGELVVRIA 85

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Search completed: October 9, 2003, 10:14:58
 Job time : 11.333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 10:09:40 ; Search time 49.333 Seconds
(without alignments)
104.616 Million cell updates/sec

Title: US-09-549-186b-8

Perfect score: 101

Sequence: 1 CGSGVGRDGSGLARVARQL 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:**
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 77 | 76.2 | 20 | 12 | Q9PXE4 |
| 2 | 71 | 70.3 | 213 | 12 | Q912L2 |
| 3 | 71 | 70.3 | 213 | 12 | Q67446 |
| 4 | 71 | 70.3 | 213 | 12 | Q67448 |
| 5 | 71 | 70.3 | 213 | 12 | Q65093 |
| 6 | 68 | 67.3 | 213 | 12 | Q98VZ6 |
| 7 | 67 | 66.3 | 210 | 12 | Q67438 |
| 8 | 67 | 66.3 | 969 | 12 | Q9Q2N6 |
| 9 | 66 | 65.3 | 169 | 12 | Q67442 |
| 10 | 65 | 64.4 | 126 | 12 | Q8V443 |
| 11 | 62 | 61.4 | 125 | 12 | Q8V442 |
| 12 | 62 | 61.4 | 143 | 12 | Q9YPU0 |
| 13 | 62 | 61.4 | 208 | 12 | Q8JUR8 |
| 14 | 62 | 61.4 | 211 | 12 | Q8JUR0 |
| 15 | 62 | 61.4 | 212 | 12 | Q8JUR1 |
| 16 | 62 | 61.4 | 213 | 12 | Q8JUS6 |

| | | | | | | |
|----|----|------|-----|----|--------|--------------------|
| 17 | 62 | 61.4 | 213 | 12 | Q8JUM1 | Q8JUM1 foot-and-mo |
| 18 | 62 | 61.4 | 213 | 12 | Q8JUQ9 | Q8JUQ9 foot-and-mo |
| 19 | 62 | 61.4 | 213 | 12 | Q8JUP7 | Q8JUP7 foot-and-mo |
| 20 | 62 | 61.4 | 213 | 12 | Q8JUP4 | Q8JUP4 foot-and-mo |
| 21 | 62 | 61.4 | 213 | 12 | Q912L1 | Q912L1 foot-and-mo |
| 22 | 62 | 61.4 | 213 | 12 | Q8JUS5 | Q8JUS5 foot-and-mo |
| 23 | 62 | 61.4 | 213 | 12 | Q8JUL1 | Q8JUL1 foot-and-mo |
| 24 | 62 | 61.4 | 213 | 12 | Q8JUN1 | Q8JUN1 foot-and-mo |
| 25 | 62 | 61.4 | 213 | 12 | Q8JUP5 | Q8JUP5 foot-and-mo |
| 26 | 62 | 61.4 | 213 | 12 | Q8JUN0 | Q8JUN0 foot-and-mo |
| 27 | 62 | 61.4 | 213 | 12 | Q8JUP3 | Q8JUP3 foot-and-mo |
| 28 | 62 | 61.4 | 213 | 12 | Q8JUQ2 | Q8JUQ2 foot-and-mo |
| 29 | 62 | 61.4 | 213 | 12 | Q8JUQ1 | Q8JUQ1 foot-and-mo |
| 30 | 62 | 61.4 | 213 | 12 | Q8JUL0 | Q8JUL0 foot-and-mo |
| 31 | 62 | 61.4 | 213 | 12 | Q8JUS7 | Q8JUS7 foot-and-mo |
| 32 | 62 | 61.4 | 213 | 12 | Q8JUM0 | Q8JUM0 foot-and-mo |
| 33 | 62 | 61.4 | 213 | 12 | Q8JUM3 | Q8JUM3 foot-and-mo |
| 34 | 62 | 61.4 | 213 | 12 | Q8JUM0 | Q8JUM0 foot-and-mo |
| 35 | 62 | 61.4 | 213 | 12 | Q8JUM8 | Q8JUM8 foot-and-mo |
| 36 | 62 | 61.4 | 213 | 12 | Q8JUR0 | Q8JUR0 foot-and-mo |
| 37 | 62 | 61.4 | 213 | 12 | Q8JUS5 | Q8JUS5 foot-and-mo |
| 38 | 60 | 59.4 | 197 | 12 | Q8JUT2 | Q8JUT2 foot-and-mo |
| 39 | 60 | 59.4 | 213 | 12 | Q8JUM4 | Q8JUM4 foot-and-mo |
| 40 | 60 | 59.4 | 652 | 12 | Q9Q2N8 | Q9Q2N8 foot-and-mo |
| 41 | 59 | 58.4 | 213 | 12 | Q8JUM9 | Q8JUM9 foot-and-mo |
| 42 | 59 | 58.4 | 213 | 12 | Q912K6 | Q912K6 foot-and-mo |
| 43 | 59 | 58.4 | 213 | 12 | Q66924 | Q66924 foot-and-mo |
| 44 | 59 | 58.4 | 213 | 12 | Q912K4 | Q912K4 foot-and-mo |
| 45 | 59 | 58.4 | 213 | 12 | Q912L0 | Q912L0 foot-and-mo |

ALIGNMENTS

RESULT 1

ID Q9PXE4 PRELIMINARY; PRT; 20 AA.
AC Q9PXE4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE VPI protein (Fragment).
OS Foot-and-mouth disease virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OX Aphanovirus.
RN NCBI_TaxID=12110;
RP [1]
RX MEDLINE=96100820; PubMed=7483796;
RA Piattelli P., Hassard S., Newman J.F., Brown F.;
RT "Antigenic variants in a plaque-isolate of foot-and-mouth disease virus: implications for vaccine production.";
RL Vaccine 13:781-784(1995).
SQ SEQUENCE 20 AA; 1925 MW; E91E87C99C19D7DB CRC64;

Query Match 76.2%; Score 77; DB 12; Length 20;
Best Local Similarity 89.5%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGSGVGRDGSGLARVARQL 20
DB 1 GSGVGRDGSGLARVARQL 19
RESULT 2
Q912L2
ID Q912L2 PRELIMINARY; PRT; 213 AA.
AC Q912L2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE VPI protein (Fragment).
GN ID.

OC Foot-and-mouth disease virus A.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12111;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A Arg/68;
RX MEDLINE=21580796; PubMed=11724271;
RA Konig G.A., Blanco C., Knowles N.J., Palma E.L., Maradei E.,
RA Piccone M.E.;
RT "Phylogenetic analysis of foot-and-mouth disease viruses isolated in
RT Argentina";
RL Virus Genes 23:175-182(2001).
DR EMBL, AJ308694; CAC48168.1; -;
DR InterPro: IPR004080; FMDVPIcoat.
DR InterPro: IPR001676; RHV.
DR Pfam: PF00073; rhv; 1.
DR PRINTS: PR01542; FMDVPIcoat.
FT NON_TER 1 1
FT SEQUENCE 213 AA; 23488 MW; 203EFCB8AB45EECE CRC64;

Query Match 70.3%; Score 71; DB 12; Length 213;
Best Local Similarity 78.9%; Pred. No. 0.0017;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 GSGVRGDFGSLARVAROL 20
Db 140 GSGRRGDMGSLARVARAKOL 158

RESULT 3

ID Q67446 PRELIMINARY; PRT; 213 AA.

AC Q67446; Q67447;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Foot and mouth disease virus (Serotype Aven/76), capsid protein VP1
DE mRNA (Fragment).
OS Foot-and-mouth disease virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12110;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85190547; PubMed=2986125;
RA Wedde11 G.N., Yansura D.G., Dowdenko D.J., Hostlin M.E., Grubman M.J.,
RA Moore D.M., Kleid D.G.;
RT "Sequence variation in the gene for the immunogenic capsid protein VP1
RT of foot-and-mouth disease virus type A";
RL Proc. Natl. Acad. Sci. U.S.A. 82:2618-2622(1985).
DR EMBL, K03344; AAA42600.1; -;
DR InterPro: IPR004080; FMDVPIcoat.
DR InterPro: IPR001676; RHV.
DR Pfam: PF00073; rhv; 1.
DR PRINTS: PR01542; FMDVPIcoat.
FT NON_TER 1 1
FT SEQUENCE 213 AA; 23311 MW; C4ED4E0116A0DB8A CRC64;

Query Match 70.3%; Score 71; DB 12; Length 213;
Best Local Similarity 78.9%; Pred. No. 0.0017;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 GSGVRGDFGSLARVAROL 20
Db 140 GSGRRGDMGSLARVARAKOL 158

RESULT 4
Q67448
ID Q67448 PRELIMINARY; PRT; 213 AA.

AC Q67448; Q67449;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Foot and mouth disease virus (Serotype Aarg/79), capsid protein VP1
DE mRNA (Fragment).
OS Foot-and-mouth disease virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12110;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85190547; PubMed=2986125;
RA Wedde11 G.N., Yansura D.G., Dowdenko D.J., Hostlin M.E., Grubman M.J.,
RA Moore D.M., Kleid D.G.;
RT "Sequence variation in the gene for the immunogenic capsid protein VP1
RT of foot-and-mouth disease virus type A";
RL Proc. Natl. Acad. Sci. U.S.A. 82:2618-2622(1985).
DR EMBL, K03345; AAA42601.1; -;
DR InterPro: IPR004080; FMDVPIcoat.
DR InterPro: IPR001676; RHV.
DR Pfam: PF00073; rhv; 1.
DR PRINTS: PR01542; FMDVPIcoat.
FT NON_TER 1 1
FT SEQUENCE 213 AA; 23345 MW; 546C7F78CD45CC0 CRC64;

Query Match 70.3%; Score 71; DB 12; Length 213;
Best Local Similarity 78.9%; Pred. No. 0.0017;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 GSGVRGDFGSLARVAROL 20
Db 140 GSGRRGDMGSLARVARAKOL 158

RESULT 5

ID Q65093 PRELIMINARY; PRT; 213 AA.

AC Q65093;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Foot and mouth disease virus strain A Venceslau VP1 (Fragment).
OS Foot-and-mouth disease virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12110;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85077620; PubMed=6096217;
RA Cheung A., Whitehead P., Weiss S., Kupper H.;
RT "Nucleotide sequence of the VP1 gene of the foot-and-mouth disease
RT virus strain A Venceslau";
RL Gene 30:241-245(1984).
DR EMBL, M12905; AAA42663.1; -;
DR InterPro: IPR004080; FMDVPIcoat.
DR InterPro: IPR001676; RHV.
DR Pfam: PF00073; rhv; 1.
DR PRINTS: PR01542; FMDVPIcoat.
FT NON_TER 1 1
FT SEQUENCE 213 AA; 23327 MW; 04808BD9571D7073 CRC64;

Query Match 70.3%; Score 71; DB 12; Length 213;
Best Local Similarity 78.9%; Pred. No. 0.0017;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 GSGVRGDFGSLARVAROL 20
Db 140 GSGRRGDMGSLARVARAKOL 158

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RESULT 6
Q98VZ6 PRELIMINARY; PRT; 213 AA.
ID Q98VZ6;
AC Q98VZ6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE VPI (Fragment).
GN 1D.
OS Foot-and-mouth disease virus A.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12111;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A76/Argentina/76;
RX MEDLINE=21580796; PubMed=11724271;
RA Konig G.A., Blanco C., Knowles N.J., Palma E.L., Maradei E.,
  "Phylogenetic analysis of foot-and-mouth disease viruses isolated in
  Argentina."
RT Virus Genes 23:175-182(2001).
RL EMBL: AJ409219; CAC34727.1; -.
DR HSP: 088571; 1TME.
DR InterPro: IPR004080; FMDVPIcoat.
DR Pfam: PF00073; rhv; 1.
DR PRINTS: PR01542; FMDVPIcoat.
FT NON_TER 1
FT NON_TER 213
SQ SEQUENCE 213 AA; 23494 MW; 92CBEDBC885F3C9 CRC64;

Query Match 67.3%; Score 68; DB 12; Length 213;
Best Local Similarity 78.9%; Pred. No. 0.0052;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 GSGVGDGSLARVROL 20
DB 140 GSGRRDMSLARVROL 158

RESULT 7
Q67438 PRELIMINARY; PRT; 210 AA.
ID Q67438;
AC Q67438;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Foot and mouth disease virus (Serotype A24), capsid protein VPI mRNA
  (Fragment).
OS Foot-and-mouth disease virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12110;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85190547; PubMed=2986125;
RA Weddell G.N., Yansura D.G., Dowbenko D.J., Hoatlin M.E., Grubman M.J.,
  Moore D.M., Kleid D.G.;
  "Sequence variation in the gene for the immunogenic capsid protein VPI
  of foot-and-mouth disease virus type A."
RT Proc. Natl. Acad. Sci. U.S.A. 82:2618-2622(1985).
RL EMBL: K03340; AAA42595.1; -.
DR InterPro: IPR004080; FMDVPIcoat.
DR Pfam: PF00073; rhv; 1.
DR PRINTS: PR01542; FMDVPIcoat.
FT NON_TER 1
FT NON_TER 210
SQ SEQUENCE 210 AA; 23089 MW; 1C96CA1C5E4F6A60 CRC64;

Query Match 66.3%; Score 67; DB 12; Length 210;
Best Local Similarity 73.7%; Pred. No. 0.0075;

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Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 GSGVGDGSLARVROL 20
DB 137 GSGRRDMSLARVROL 155

RESULT 8
Q9Q2N6 PRELIMINARY; PRT; 969 AA.
ID Q9Q2N6;
AC Q9Q2N6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE Polypeptide (Fragment).
OS Foot-and-mouth disease virus A.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12111;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A24/Cruzeiro/Brazil/55;
RA Abrams C.C.;
  "Nucleotide sequence of foot-and-mouth disease virus
  A24/Cruzeiro/Brazil/55 from the POLY(C) tract to 2B."
RT Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A24/Cruzeiro/Brazil/55;
RA Knowles N.J., Samuel A.R., Aktas S., Rowe C.A., Abrams C.C.,
  Newman J.W.I., King A.M.Q.;
  "Phylogenetic comparison of the capsid-coding region of all seven
  foot-and-mouth disease virus serotypes."
RT Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
RL EMBL: AF251476; CAB6583.1; -.
DR HSP: 088571; 1TME.
DR MEROPS: C28.001; -.
DR InterPro: IPR004080; FMDVPIcoat.
DR Pfam: PF00073; rhv; 3.
DR PRINTS: PR01542; FMDVPIcoat.
FT CHAIN 1 >201 LEADER.
FT CHAIN 202 >286 1A (VP4).
FT CHAIN 287 >504 1B (VP2).
FT CHAIN 505 >725 1C (VP3).
FT CHAIN 726 >938 1D (VP1).
FT CHAIN 939 >954 2A.
FT CHAIN 955 >969 2B.
FT NON_TER 969
SQ SEQUENCE 969 AA; 107629 MW; 7DD5D908FCFF89FD CRC64;

Query Match 66.3%; Score 67; DB 12; Length 969;
Best Local Similarity 73.7%; Pred. No. 0.0041;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 GSGVGDGSLARVROL 20
DB 865 GSGRRDMSLARVROL 883

RESULT 9
Q67442 PRELIMINARY; PRT; 169 AA.
ID Q67442;
AC Q67442;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Foot and mouth disease virus (Serotype A32), capsid protein VPI mRNA
  (Fragment).
OS Foot-and-mouth disease virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12110;

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[1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE-85190547; PubMed-2968125;
 RA Wedge D.G., Yansura D.G., Dowbenko D.J., Hoatlin M.E., Grubman M.J.,
 RT Moore D.M., Kleid D.G.;
 "Sequence variation in the gene for the immunogenic capsid protein VP1
 of foot-and-mouth disease virus type A.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:2618-2622(1985).
 DR EMBL; K03342; AAA42598.1; -;
 DR HSSP; Q88571; 1TME.
 DR InterPro; IPR004080; FMDVpicoat.
 DR InterPro; IPR001676; Rhv.
 DR Pfam; PF00073; rhv; 2
 DR PRINTS; PR01542; FMDVpicoat.
 FT NON_TER 1 1
 FT NON_TER 169 169
 SQ SEQUENCE 169 AA; 18499 MW; 9E8AEDC94AC57F67 CRC64;

Query Match 65.3%; Score 66; DB 12; Length 169;
 Best Local Similarity 73.7%; Pred. No. 0.0085;
 Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 GSGVGFSGSLARVROL 20
 DB 96 GSGRGDLGSLARVAKOL 114

RESULT 10

O8V443 PRELIMINARY; PRT; 126 AA.
 ID O8V443
 AC O8V443
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Vp1 (Fragment).
 OS Foot-and-mouth disease virus A.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
 CC Aphthovirus
 NCBI_TaxID=12111;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-KER/1/76;
 RA van Rensburg H.G., Bastos A.D., Haydon D., Joubert F., Nel L.H.;
 RT "Gene heterogeneity in the leader and 3c proteinases of foot-and-mouth
 disease virus.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF390861; AAL73359.1; -;
 DR InterPro; IPR004080; FMDVpicoat.
 DR InterPro; IPR001676; Rhv.
 DR Pfam; PF00073; rhv; 1.
 DR PRINTS; PR01542; FMDVpicoat.
 FT NON_TER 1 1
 FT NON_TER 126 126
 SQ SEQUENCE 126 AA; 13693 MW; 82675FAC45F713BB CRC64;

Query Match 64.4%; Score 65; DB 12; Length 126;
 Best Local Similarity 77.8%; Pred. No. 0.009;
 Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 GSGVGFSGSLARVROL 20
 DB 54 GSGRGDLGSLARVAKOL 71

RESULT 11

O8V442 PRELIMINARY; PRT; 125 AA.
 ID O8V442
 AC O8V442
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Vp1 (Fragment).
 OS Foot-and-mouth disease virus A.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
 CC Aphthovirus.
 NCBI_TaxID=12111;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-GAM/51/98;
 RA van Rensburg H.G., Bastos A.D., Haydon D., Joubert F., Nel L.H.;
 RT "Gene heterogeneity in the leader and 3c proteinases of foot-and-mouth
 disease virus.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF390862; AAL73360.1; -;
 DR InterPro; IPR004080; FMDVpicoat.
 DR InterPro; IPR001676; Rhv.
 DR Pfam; PF00073; rhv; 1.
 DR PRINTS; PR01542; FMDVpicoat.
 FT NON_TER 1 1
 FT NON_TER 125 125
 SQ SEQUENCE 125 AA; 13486 MW; 2D172B9F0C281A02 CRC64;

Query Match 61.4%; Score 62; DB 12; Length 125;
 Best Local Similarity 73.7%; Pred. No. 0.027;
 Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

RESULT 12

O9YPU0 PRELIMINARY; PRT; 143 AA.
 ID O9YPU0
 AC O9YPU0
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Vp1 protein (Fragment).
 CN Vp1.
 OS Foot-and-mouth disease virus A.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
 CC Aphthovirus.
 NCBI_TaxID=12111;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NM/XZ/64;
 RA Liu Z., Zhao Q., Liu W., Xie Q.;
 RT "Analysis of Vp1 coding nucleotide sequences of six strains of foot-
 and-mouth disease virus type A.";
 RL Ping Tu Hsueh Pao 14:60-67(1998).
 DR EMBL; AJ131664; CAA10474.1; -;
 DR InterPro; IPR004080; FMDVpicoat.
 DR InterPro; IPR001676; Rhv.
 DR Pfam; PF00073; rhv; 1.
 DR PRINTS; PR01542; FMDVpicoat.
 FT NON_TER 1 1
 FT NON_TER 143 143
 SQ SEQUENCE 143 AA; 15881 MW; CF0CC1858CC331E0 CRC64;

Query Match 61.4%; Score 62; DB 12; Length 143;
 Best Local Similarity 72.2%; Pred. No. 0.032;
 Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 3 GSGVGFSGSLARVROL 20
 DB 71 AGRRGDLGSLARVAKOL 88

RESULT 13

O8JUR8 PRELIMINARY; PRT; 208 AA.
 ID O8JUR8
 AC O8JUR8
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE 1D protein (Fragment).
GN POL.
OS Foot-and-mouth disease virus A.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12111;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A/IND/170/88;
RX MEDLINE=21954626; PubMed=11958451;
RA Tosh C., Sanyal A., Hemadri D., Venkataraman R.;
RT "Phylogenetic analysis of serotype A foot-and-mouth disease virus isolated in India between 1977 and 2000.";
RL Arch. Virol. 147:493-513(2002).
DR EMBL; AF390612; AAM63984.1; -;
DR InterPro; IPR004080; FMDVpicoat.
DR Pfam; PF00073; rhv.1.
DR PRINTS; PRO1542; FMDVpicoat.
FT NON_TER 1
SQ SEQUENCE 208 AA; 22607 MW; 6CE616F86E60CF7E CRC64;
OY Query Match 61.4%; Score 62; DB 12; Length 208;
Best Local Similarity 68.4%; Pred. No. 0.048;
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
OY 2 GSGVGDGSLALRVAROL 20
DB 140 GTGRRGDLGALAAVAAOL 158
RESULT 14
O8JUP0 PRELIMINARY; PRT; 211 AA.
AC O8JUP0.
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE 1D protein (Fragment).
GN POL.
OS Foot-and-mouth disease virus A.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12111;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A/IND/302/88;
RX MEDLINE=21954626; PubMed=11958451;
RA Tosh C., Sanyal A., Hemadri D., Venkataraman R.;
RT "Phylogenetic analysis of serotype A foot-and-mouth disease virus isolated in India between 1977 and 2000.";
RL Arch. Virol. 147:493-513(2002).
DR EMBL; AF390641; AAM64012.1; -;
DR InterPro; IPR004080; FMDVpicoat.
DR Pfam; PF00073; rhv.1.
DR PRINTS; PRO1542; FMDVpicoat.
FT NON_TER 1
SQ SEQUENCE 211 AA; 23100 MW; CFBFC94CCD9E2FE3 CRC64;
OY Query Match 61.4%; Score 62; DB 12; Length 211;
Best Local Similarity 68.4%; Pred. No. 0.049;
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
OY 2 GSGVGDGSLALRVAROL 20
DB 140 GTGRRGDLGALAAVAAOL 158
RESULT 15
O8JUP1

ID O8JUP1 PRELIMINARY; PRT; 212 AA.
AC O8JUP1;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE 1D protein (Fragment).
GN POL.
OS Foot-and-mouth disease virus A.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12111;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A/IND/299/99;
RX MEDLINE=21954626; PubMed=11958451;
RA Tosh C., Sanyal A., Hemadri D., Venkataraman R.;
RT "Phylogenetic analysis of serotype A foot-and-mouth disease virus isolated in India between 1977 and 2000.";
RL Arch. Virol. 147:493-513(2002).
DR EMBL; AF390640; AAM64011.1; -;
DR InterPro; IPR004080; FMDVpicoat.
DR Pfam; PF00073; rhv.1.
DR PRINTS; PRO1542; FMDVpicoat.
FT NON_TER 1
SQ SEQUENCE 212 AA; 23150 MW; E6B690890042CD3A CRC64;
OY Query Match 61.4%; Score 62; DB 12; Length 212;
Best Local Similarity 68.4%; Pred. No. 0.049;
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
OY 2 GSGVGDGSLALRVAROL 20
DB 139 GTGRRGDLGALAAVAAOL 157

Search completed: October 9, 2003, 10:17:34
Job time : 49.333 secs

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OM protein - protein search, using sw model

Run on: October 9, 2003, 10:11:24 ; Search time 17.333 Seconds
(without alignments)
48.820 Million cell updates/sec

Title: US-09-549-186b-8

Perfect score: 101

Sequence: 1 CGSGVGRDPSGLALRYARQL 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents.AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCPMUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile01.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|---------------------|-------------------|
| 1 | 101 | 100.0 | 20 | 4 US-08-716-249-8 | Sequence 8, Appl |
| 2 | 94 | 93.1 | 20 | 4 US-08-716-249-7 | Sequence 7, Appl |
| 3 | 93 | 92.1 | 20 | 4 US-08-716-249-9 | Sequence 9, Appl |
| 4 | 85 | 84.2 | 35 | 3 US-09-100-600A-1 | Sequence 1, Appl |
| 5 | 85 | 84.2 | 46 | 3 US-09-100-600A-38 | Sequence 38, Appl |
| 6 | 85 | 84.2 | 75 | 3 US-09-100-600A-28 | Sequence 28, Appl |
| 7 | 83 | 82.2 | 31 | 1 US-08-418-716A-3 | Sequence 3, Appl |
| 8 | 82 | 81.2 | 31 | 1 US-08-418-716A-4 | Sequence 4, Appl |
| 9 | 81 | 80.2 | 31 | 1 US-08-418-716A-5 | Sequence 5, Appl |
| 10 | 81 | 80.2 | 31 | 1 US-08-418-716A-6 | Sequence 6, Appl |
| 11 | 79.5 | 78.7 | 19 | 4 US-08-716-249-2 | Sequence 2, Appl |
| 12 | 79 | 78.2 | 19 | 4 US-08-716-249-1 | Sequence 1, Appl |
| 13 | 78.5 | 77.7 | 31 | 1 US-08-418-716A-1 | Sequence 7, Appl |
| 14 | 78 | 77.2 | 31 | 1 US-08-418-716A-7 | Sequence 7, Appl |
| 15 | 78 | 77.2 | 31 | 1 US-08-418-716A-7 | Sequence 7, Appl |
| 16 | 77 | 76.2 | 35 | 3 US-09-100-600A-2 | Sequence 2, Appl |
| 17 | 77 | 76.2 | 46 | 3 US-09-100-600A-3 | Sequence 3, Appl |
| 18 | 77 | 76.2 | 65 | 3 US-09-100-600A-27 | Sequence 27, Appl |
| 19 | 77 | 76.2 | 75 | 3 US-09-100-600A-29 | Sequence 29, Appl |
| 20 | 71 | 70.3 | 35 | 3 US-09-100-600A-8 | Sequence 8, Appl |
| 21 | 71 | 70.3 | 46 | 3 US-09-100-600A-42 | Sequence 42, Appl |
| 22 | 71 | 70.3 | 46 | 3 US-09-100-600A-49 | Sequence 49, Appl |
| 23 | 71 | 70.3 | 46 | 3 US-09-100-600A-50 | Sequence 50, Appl |
| 24 | 67 | 66.3 | 46 | 3 US-09-100-600A-43 | Sequence 43, Appl |
| 25 | 67 | 66.3 | 46 | 3 US-09-100-600A-44 | Sequence 44, Appl |
| 26 | 67 | 66.3 | 46 | 3 US-09-100-600A-48 | Sequence 48, Appl |
| 27 | 66 | 65.3 | 46 | 3 US-09-100-600A-45 | Sequence 45, Appl |

| | | | | | |
|----|----|------|-----|------------------------|-------------------|
| 28 | 63 | 62.4 | 35 | 3 US-09-100-600A-9 | Sequence 9, Appl |
| 29 | 63 | 62.4 | 55 | 3 US-09-100-600A-33 | Sequence 33, Appl |
| 30 | 60 | 59.4 | 46 | 3 US-09-100-600A-39 | Seq. acc 39, Appl |
| 31 | 59 | 58.4 | 46 | 3 US-09-100-600A-46 | Sequence 46, Appl |
| 32 | 55 | 54.5 | 45 | 3 US-09-100-600A-55 | Sequence 55, Appl |
| 33 | 54 | 53.5 | 46 | 3 US-09-100-600A-47 | Sequence 47, Appl |
| 34 | 53 | 52.5 | 45 | 3 US-09-100-600A-60 | Sequence 60, Appl |
| 35 | 50 | 49.5 | 45 | 3 US-09-100-600A-61 | Sequence 61, Appl |
| 36 | 50 | 49.5 | 45 | 3 US-09-100-600A-62 | Sequence 62, Appl |
| 37 | 50 | 49.5 | 45 | 3 US-09-100-600A-64 | Sequence 64, Appl |
| 38 | 50 | 49.5 | 45 | 3 US-09-100-600A-65 | Sequence 65, Appl |
| 39 | 50 | 49.5 | 46 | 3 US-09-100-600A-40 | Sequence 40, Appl |
| 40 | 50 | 49.5 | 46 | 3 US-09-100-600A-41 | Sequence 41, Appl |
| 41 | 48 | 47.5 | 45 | 3 US-09-100-600A-56 | Sequence 56, Appl |
| 42 | 47 | 46.5 | 170 | 4 US-09-732-210-1676 | Sequence 1676, Ap |
| 43 | 47 | 46.5 | 387 | 4 US-09-252-991A-17881 | Sequence 17881, A |
| 44 | 46 | 45.5 | 45 | 3 US-09-100-600A-52 | Sequence 52, Appl |
| 45 | 46 | 45.5 | 54 | 3 US-09-100-600A-34 | Sequence 34, Appl |

ALIGNMENTS

RESULT 1
US-08-716-249-8
Sequence 8, Application US/08716249
Patent No. 6455244
GENERAL INFORMATION:
APPLICANT: Guichard, Gilles
APPLICANT: Muller, Sylviane
APPLICANT: Briand, Jean-Paul
APPLICANT: Regemortel, Marc
TITLE OF INVENTION: Retropeptides, Antibodies Thereof, and
TITLE OF INVENTION: Uses Thereof for Vaccination and In Vitro Diagnosis
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Spencer & Frank
STREET: 1100 New York Avenue, Suite 300E
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,249
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/00292
FILING DATE: 13-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Calvetti, Frederick F.
REGISTRATION NUMBER: 28,557
REFERENCE/DOCKET NUMBER: GROFO 7001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)414-4000
TELEFAX: (202)414-4040
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-716-249-8
Query Match 100.0%; Score 101; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGSGVRGDFGSLALRYARQL 20
Db 1 CGSGVRGDFGSLALRYARQL 20

RESULT 2

US-08-716-249-7
; Sequence 7, Application US/08716249
; Patent No. 6455244
; GENERAL INFORMATION:
; APPLICANT: Guichard, Gilles
; APPLICANT: Muller, Sylviane
; APPLICANT: Briand, Jean-Paul
; APPLICANT: Regemortel, Marc
; TITLE OF INVENTION: Retropeptides, Antibodies Thereeto, and
; TITLE OF INVENTION: Uses Thereof for Vaccination and In Vitro Diagnosis
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spencer & Frank
; STREET: 1100 New York Avenue, Suite 300E
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,249
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/00292
; FILING DATE: 13-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Calvetti, Frederick F.
; REGISTRATION NUMBER: 28,557
; REFERENCE/DOCKET NUMBER: GROFO 7001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)414-4000
; TELEFAX: (202)414-4040
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-08-716-249-7

Query Match 93.1%; Score 94; DB 4; Length 20;

Best Local Similarity 95.0%; Pred. No. 2.6e-08; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGSGVRGDFGSLALRYARQL 20
Db 1 CGSGVRGDFGSLALRYARQL 20

RESULT 3
US-08-716-249-9
; Sequence 9, Application US/08716249
; Patent No. 6455244
; GENERAL INFORMATION:
; APPLICANT: Guichard, Gilles
; APPLICANT: Muller, Sylviane
; APPLICANT: Briand, Jean-Paul
; APPLICANT: Regemortel, Marc
; TITLE OF INVENTION: Retropeptides, Antibodies Thereeto, and
; TITLE OF INVENTION: Uses Thereof for Vaccination and In Vitro Diagnosis

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spencer & Frank
STREET: 1100 New York Avenue, Suite 300E
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,249
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/00292
FILING DATE: 13-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Calvetti, Frederick F.
REGISTRATION NUMBER: 28,557
REFERENCE/DOCKET NUMBER: GROFO 7001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)414-4000
TELEFAX: (202)414-4040
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: YES
ANTI-SENSE: YES
US-08-716-249-9

Query Match 92.1%; Score 93; DB 4; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.7e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGSGVRGDFGSLALRYARQL 20
Db 1 CGSGVRGDFGSLALRYARQL 20

RESULT 4

US-09-100-600A-1
; Sequence 1, Application US/09100600A
; Patent No. 6107021
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Y1
; APPLICANT: Shen, Ming
; TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR
; TITLE OF INVENTION: FOOT-AND-MOUTH DISEASE
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Flinnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,600A
; FILING DATE: 20-Jun-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin

REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4156
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-600A-1

Query Match 84.2%; Score 85; DB 3; Length 35;
Best Local Similarity 94.7%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGVGDGFGSLAPRVARQL 20
DB 7 GSGVGDGFGSLAPRVARQL 25

RESULT 5
US-09-100-600A-38
Sequence 38, Application US/09100600A
Patent No. 6107021
GENERAL INFORMATION:
APPLICANT: Wang, Chang YI
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR
NUMBER OF INVENTION: FOOT-AND-MOUTH DISEASE
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,600A
FILING DATE: 20-Jun-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4156
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-600A-38

Query Match 84.2%; Score 85; DB 3; Length 46;
Best Local Similarity 94.7%; Pred. No. 1.6e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGVGDGFGSLAPRVARQL 20
DB 16 GSGVGDGFGSLAPRVARQL 34

RESULT 6

US-09-100-600A-28
Sequence 28, Application US/09100600A
Patent No. 6107021
GENERAL INFORMATION:
APPLICANT: Wang, Chang YI
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR
NUMBER OF INVENTION: FOOT-AND-MOUTH DISEASE
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Flinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,600A
FILING DATE: 20-Jun-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4156
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-600A-28

Query Match 84.2%; Score 85; DB 3; Length 75;
Best Local Similarity 94.7%; Pred. No. 2.6e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGVGDGFGSLAPRVARQL 20
DB 47 GSGVGDGFGSLAPRVARQL 65

RESULT 7
US-08-418-716A-3
Sequence 3, Application US/08418716A
Patent No. 5612040
GENERAL INFORMATION:
APPLICANT: Mason, Peter W.
APPLICANT: Baxt, Barry
APPLICANT: Reider, Elizabeth
APPLICANT: Bernstein, Anella
APPLICANT: Kang, Angray S
TITLE OF INVENTION: NO. 5612040-Infectious Foot-and-Mouth Disease
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janelle S. Graeter
STREET: Rm. 411, Bldg. 005, BARC-W
CITY: Beltsville
STATE: Maryland
COUNTRY: USA
ZIP: 20705
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,716A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Graeter, Janelle S.
REGISTRATION NUMBER: 35,024
REFERENCE/DOCKET NUMBER: 0137.94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 504-5060
TELEFAX: (301) 504-50629
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Foot and mouth disease virus
US-08-418-716A-3

Query Match 82.2%; Score 83; DB 1; Length 31;
Best Local Similarity 94.7%; Pred. No. 2.1e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGVRGDFGSLARVARQL 20
Db 11 GSGVRGDFGSLARVARQL 29

RESULT 8
US-08-418-716A-4
Sequence 4, Application US/08418716A
Patent No. 5612040
GENERAL INFORMATION:
APPLICANT: Mason, Peter W.
APPLICANT: Baxt, Barry
APPLICANT: Reider, Elizabeth
APPLICANT: Berinstein, Analia
APPLICANT: Kang, Angray S
TITLE OF INVENTION: No. 5612040-Infectious Foot-and-Mouth Disease
TITLE OF INVENTION: Viruses
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janelle S. Graeter
STREET: Rm. 411, Bldg. 005, BARC-W
CITY: Beltsville
STATE: Maryland
COUNTRY: USA
ZIP: 20705
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,716A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Graeter, Janelle S.
REGISTRATION NUMBER: 35,024
REFERENCE/DOCKET NUMBER: 0137.94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 504-50629
TELEFAX: (301) 504-5060
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Foot and mouth disease virus
US-08-418-716A-4

Query Match 81.2%; Score 82; DB 1; Length 31;
Best Local Similarity 89.5%; Pred. No. 3e-06;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGVRGDFGSLARVARQL 20
Db 11 GSGVRGDFGSLARVARQL 29

RESULT 9
US-08-418-716A-5
Sequence 5, Application US/08418716A
Patent No. 5612040
GENERAL INFORMATION:
APPLICANT: Mason, Peter W.
APPLICANT: Baxt, Barry
APPLICANT: Reider, Elizabeth
APPLICANT: Berinstein, Analia
APPLICANT: Kang, Angray S
TITLE OF INVENTION: No. 5612040-Infectious Foot-and-Mouth Disease
TITLE OF INVENTION: Viruses
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janelle S. Graeter
STREET: Rm. 411, Bldg. 005, BARC-W
CITY: Beltsville
STATE: Maryland
COUNTRY: USA
ZIP: 20705
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,716A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Graeter, Janelle S.
REGISTRATION NUMBER: 35,024
REFERENCE/DOCKET NUMBER: 0137.94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 504-50629
TELEFAX: (301) 504-5060
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Foot and mouth disease virus
US-08-418-716A-5

Query Match 80.2%; Score 81; DB 1; Length 31;
Best Local Similarity 89.5%; Pred. No. 4.3e-06;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGVRGDFGSLARVARQL 20

Db 11 GSGVGEFGSLAPVAROL 29

```

RESULT 10
US-08-418-716A-6
; Sequence 6, Application US/08418716A
; Patent No. 5612040
; GENERAL INFORMATION:
; APPLICANT: Mason, Peter W.
; APPLICANT: Baxt, Barry
; APPLICANT: Reider, Elizabeth
; APPLICANT: Bernstein, Analia
; APPLICANT: Kang, Andray S
; TITLE OF INVENTION: No. 5612040-Infectious Foot-and-Mouth Disease
; TITLE OF INVENTION: Viruses
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janelle S. Graeter
; STREET: Rm. 411, Bldg. 005, BARC-W
; CITY: Beltsville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20705
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/418,716A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Graeter, Janelle S.
; REGISTRATION NUMBER: 35,024
; REFERENCE/DOCKET NUMBER: 0137.94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 504-6629
; TELEFAX: (301) 504-5060
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE:
; ORGANISM: Foot and mouth disease virus
; US-08-418-716A-6

Query Match 80.2%; Score 81; DB 1; Length 31;
Best Local Similarity 89.5%; Pred. No. 4.3e-06;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGVGEFGSLAPVAROL 20
Db 11 GSGVGEFGSLAPVAROL 29

RESULT 11
US-08-716-249-2
; Sequence 2, Application US/08716249
; Patent No. 6455244
; GENERAL INFORMATION:
; APPLICANT: Guichard, Gilles
; APPLICANT: Muller, Sylviane
; APPLICANT: Briand, Jean-Paul
; APPLICANT: Regemortel, Marc
; TITLE OF INVENTION: Retropeptides, Antibodies Thereto, and
; TITLE OF INVENTION: Uses Thereof for Vaccination and In Vitro Diagnosis
```

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; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spencer & Frank
; STREET: 1100 New York Avenue, Suite 300E
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,249
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/00292
; FILING DATE: 13-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Calvetti, Frederick F.
; REGISTRATION NUMBER: 28,557
; REFERENCE/DOCKET NUMBER: GROFO 7001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)414-4000
; TELEFAX: (202)414-4040
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-716-249-2

Query Match 78.7%; Score 79.5; DB 4; Length 19;
Best Local Similarity 90.0%; Pred. No. 4.4e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 CGSGVRDGFSLAPVAROL 20
Db 1 CGSGVRDGFSLAPVAROL 19

RESULT 12
US-08-418-716A-2
; Sequence 2, Application US/08418716A
; Patent No. 5612040
; GENERAL INFORMATION:
; APPLICANT: Mason, Peter W.
; APPLICANT: Baxt, Barry
; APPLICANT: Reider, Elizabeth
; APPLICANT: Bernstein, Analia
; APPLICANT: Kang, Andray S
; TITLE OF INVENTION: No. 5612040-Infectious Foot-and-Mouth Disease
; TITLE OF INVENTION: Viruses
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janelle S. Graeter
; STREET: Rm. 411, Bldg. 005, BARC-W
; CITY: Beltsville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20705
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/418,716A
; FILING DATE:
```

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Graeter, Janelle S.
REGISTRATION NUMBER: 35,024
REFERENCE/DOCKET NUMBER: 0137.94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 504-6629
TELEFAX: (301) 504-5060
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Foot and mouth disease virus
US-08-418-716A-2

Query Match 78.2%; Score 79; DB 1; Length 31;
Best Local Similarity 89.5%; Pred. No. 8.8e-06;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GSGVRGDFGSLARVAROL 20
||| ||||| |||||
DB 11 GSGVRGDFGSLARVAROL 29

RESULT 13
US-08-716-249-1
Sequence 1, Application US/08716249
GENERAL INFORMATION:
APPLICANT: Guichard, Gilles
APPLICANT: Muller, Sylviane
APPLICANT: Briand, Jean-Paul
APPLICANT: Regemortel, Marc
TITLE OF INVENTION: Retropeptides, Antibodies Thereof, and
TITLE OF INVENTION: Uses Thereof for Vaccination and In Vitro Diagnosis
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSES:
ADDRESSER: Spencer & Frank
STREET: 1100 New York Avenue, Suite 300E
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,249
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/00292
FILING DATE: 13-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Calvetti, Frederick F.
REGISTRATION NUMBER: 28,557
REFERENCE/DOCKET NUMBER: GROFO 7001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)414-4000
TELEFAX: (202)414-4040
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-716-249-1

Query Match 77.7%; Score 78.5; DB 4; Length 19;
Best Local Similarity 90.0%; Pred. No. 6.3e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 CGSGVRGDFGSLARVAROL 20
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DB 1 CGSGVRGDFGSLARVAROL 19

RESULT 14
US-08-418-716A-1
Sequence 1, Application US/08418716A
Patent No. 5612040
GENERAL INFORMATION:
APPLICANT: Mason, Peter W.
APPLICANT: Baxt, Barry
APPLICANT: Reider, Elizabeth
APPLICANT: Bernstein, Analia
APPLICANT: Kang, Angray S
TITLE OF INVENTION: No. 5612040-Infectious Foot-and-Mouth Disease
TITLE OF INVENTION: Viruses
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSER: Janelle S. Graeter
STREET: Rm. 411, Bldg. 005, BARC-W
CITY: Beltsville
STATE: Maryland
COUNTRY: USA
ZIP: 20705

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,716A
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Graeter, Janelle S.
REGISTRATION NUMBER: 35,024
REFERENCE/DOCKET NUMBER: 0137.94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 504-6629
TELEFAX: (301) 504-5060
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Foot and mouth disease virus
US-08-418-716A-1

Query Match 77.2%; Score 78; DB 1; Length 31;
Best Local Similarity 89.5%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GSGVRGDFGSLARVAROL 20
||| ||||| |||||
DB 11 GSGVRGDFGSLARVAROL 29

RESULT 15
US-08-418-716A-7

; Sequence 7, Application US/08418716A
; Patent No. 5612040
; GENERAL INFORMATION:
; APPLICANT: Mason, Peter W.
; APPLICANT: Baxt, Barry
; APPLICANT: Reider, Elizabeth
; APPLICANT: Berlnstein, Analia
; APPLICANT: Kang, Angray S
; TITLE OF INVENTION: No. 5612040-Infectious Foot-and-Mouth Disease
; TITLE OF INVENTION: Viruses
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janelle S. Graeter
; STREET: Rm. 411, Bldg. 005, BARC-W
; CITY: Beltsville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20705
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/418,716A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Graeter, Janelle S.
; REGISTRATION NUMBER: 35,024
; REFERENCE/DOCKET NUMBER: 0137.94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 504-6629
; TELEFAX: (301) 504-5060
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE:
; ORGANISM: Foot and mouth disease virus
; US-08-418-716A-7

Query Match 77.2%; Score 78; DB 1; Length 31;
Best Local Similarity 84.2%; Pred. No. 1.3e-05;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGVGRDGFGLRVARQL 20
||||:|||||
Db 11 GSGVKGEGSLAPRVARQL 29

Search completed: October 9, 2003, 10:19:38
Job time : 18.3333 secs

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; Sequence 9294, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9294
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9294

Query Match 42.6%; Score 43; DB 15; Length 261;
Best Local Similarity 52.6%; Pred. No. 54;
Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 2 GSGVGRDGFSLARARQL 20
Db 97 GOSVLDIDGTAYRLARQL 115

RESULT 3
US-10-102-806-595
; Sequence 595, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 595
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (269)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (278)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-595

Query Match 42.6%; Score 43; DB 15; Length 294;
Best Local Similarity 53.3%; Pred. No. 61;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 3 SGVRGDFGSLARARQL 17
Db 159 SGTSGDGLVLRARQL 173

RESULT 4
US-10-207-655-186
; Sequence 186, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 186
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-186

Query Match 42.6%; Score 43; DB 15; Length 312;
Best Local Similarity 61.5%; Pred. No. 65;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGSGVRGDFGSLA 13
Db 164 CGSGARCGDGEVA 176

RESULT 5
US-09-847-208-53
; Sequence 53, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67,002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Candida albicans (Yeast)
US-09-847-208-53

Query Match 41.6%; Score 42; DB 11; Length 350;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 3 SGVRGDFGSLARARQL 20
Db 179 SGAGGGLSLAVYARAR 196

RESULT 6
US-09-291-299A-3
; Sequence 3, Application US/09291299A
; Patent No. US20020076405A1
; GENERAL INFORMATION:
; APPLICANT: Yong, Xie
; TITLE OF INVENTION: Antigenized Antibody Vaccine for Foot-and-Mouth Disease
; FILE REFERENCE: 09/291,299
; CURRENT APPLICATION NUMBER: US/09/291,299A
; CURRENT FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 476

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; TYPE: PRT
; ORGANISM: Sus sp.
US-09-291-299A-3

Query Match
  Best Local Similarity 41.6%; Score 42; DB 9; Length 476;
  Matches 11; Conservative 2; Mismatches 7; Indels 2; Gaps 1;

QY      1 CGS--GVRGDFGSLARVROL 20
Db      115 CGKVPNLRGDLQVLAOKVARTL 136

RESULT 7
US-10-072-152-6
; Sequence 6, Application US/10072152
; Publication No. US20020142438A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Lene N.
; APPLICANT: Schuilein, Martin
; APPLICANT: Lange, Niels E.
; APPLICANT: Bjornvad, Mads E.
; APPLICANT: Moller, Soren
; APPLICANT: Glad, Sanne O. S.
; APPLICANT: Kauppinen, Markus S.
; APPLICANT: Schnorr, Kirk
; APPLICANT: Kongsbak, Lars
; TITLE OF INVENTION: No. US20020142438A1el Pectate Lyases
; FILE REFERENCE: 5378-200-US
; CURRENT APPLICATION NUMBER: US/10/072.152
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: US/09/198,955
; PRIOR FILING DATE: 1998-11-24
; PRIOR APPLICATION NUMBER: 1343/97
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 1344/97
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/067,249
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: 60/067,240
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: 09/073,684
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 09/184,217
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-072-152-6

Query Match
  Best Local Similarity 41.6%; Score 42; DB 14; Length 509;
  Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      2 GSGVRGDFGSLARV 16
Db      266 GGCTRGDFGSLARL 280

RESULT 8
US-10-222-100-3
; Sequence 3, Application US/10222100
; Publication No. US20030059439A1
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut Voor Biotechnologie VZW
; APPLICANT: Revets, Hilde
; APPLICANT: Cornelis, Pierre
; APPLICANT: De Baetselier, Patrick
; TITLE OF INVENTION: THI INDUCING NATURAL ADJUVANT FOR HETEROLOGOUS ANTIGENS
; FILE REFERENCE: 2676-5449US
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; CURRENT APPLICATION NUMBER: US/10/222.100
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: PCT/EP01/01673
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Opr1-3d-FMDV15 fusion
US-10-222-100-3

Query Match
  Best Local Similarity 41.6%; Score 42; DB 15; Length 627;
  Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      3 SGVRGDFGSLARVROL 20
Db      573 SNLRGDLQVLAOKVARTL 590

RESULT 9
US-09-738-626-6262
; Sequence 6262, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6262
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6262

Query Match
  Best Local Similarity 41.1%; Score 41.5; DB 10; Length 446;
  Matches 11; Conservative 2; Mismatches 4; Indels 3; Gaps 1;

QY      4 GVR---GDFGSLARVROL 20
Db      261 GVRIDSGDLGVLAOKVARKQL 280

RESULT 10
US-10-106-698-7642
; Sequence 7642, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
; FILE REFERENCE: PA005PI
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; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 7642
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (49)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (54)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-106-698-7642
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Query Match          40.6%; Score 41; DB 15; Length 74;
Best Local Similarity 57.9%; Pred. No. 29;
Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;
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QY      1 CGSG--VRGDFGSLARVA 17
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Db      26 CGSSRDLDHSGSLALSYA 44
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RESULT 11
US-09-815-242-11926
; Sequence 11926, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; TITLE OF INVENTION: Identification of Essential Genes In
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11926
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-815-242-11926
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Query Match          40.6%; Score 41; DB 9; Length 337;
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Best Local Similarity 47.1%; Pred. No. 1.5e+02;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY      4 GVRGDFGSLARVAROL 20
        |  |  |||  |||||
Db      157 GAAGVGSLIVQAROL 173
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RESULT 12
US-10-156-761-14684
; Sequence 14684, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OKURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIRAMA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, TOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 14684
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
; US-10-156-761-14684
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Query Match          40.6%; Score 41; DB 15; Length 394;
Best Local Similarity 52.6%; Pred. No. 1.7e+02;
Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
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QY      2 GSGVRGDFGSLARVAROL 20
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Db      192 GSGVLDLASHGVDLARFL 210
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RESULT 13
US-10-128-713A-2
; Sequence 2, Application US/10128713A
; Publication No. US20030170847A1
; GENERAL INFORMATION:
; APPLICANT: Bramucci, Michael G
; TITLE OF INVENTION: Genes Involved In Isoprenoid Compound Production
; FILE REFERENCE: CL-1788
; CURRENT APPLICATION NUMBER: US/10/128,713A
; CURRENT FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Rhodococcus erythropolis
; US-10-128-713A-2
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Query Match          40.6%; Score 41; DB 12; Length 648;
Best Local Similarity 44.0%; Pred. No. 3e+02;
Matches 11; Conservative 2; Mismatches 4; Indels 8; Gaps 1;
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QY      4 GVRGD-----FGSLARVAROL 20
        |  |||  |  |||||  |  |
Db      500 GERGVLLVAVGPFASLAEIAERT 524
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RESULT 14
US-10-128-870-23
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 10:02:18 ; Search time 58.3333 Seconds
(without alignments)
54.421 Million cell updates/sec

Title: US-09-549-186b-9

Perfect score: 99
Sequence: 1 CGSGVRGDSGLLRVARQL 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
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| 1 | 90 | 90.9 | 20 14 AAR38543 | Foot and Mouth Dis |
| 2 | 90 | 90.9 | 20 14 AAR41793 | Foot and Mouth Dis |
| 3 | 86 | 86.9 | 31 18 AAW17085 | Foot and mouth dis |
| 4 | 84 | 84.8 | 19 24 ABU08643 | Foot and mouth dis |
| 5 | 77 | 77.8 | 19 24 ABU08642 | Foot and mouth dis |
| 6 | 77 | 77.8 | 20 21 AAY94587 | Envelope gene epit |
| 7 | 77 | 77.8 | 31 4 AAP30107 | Sequence of VP1 ca |
| 8 | 77 | 77.8 | 31 6 AAP50728 | Foot-and-mouth dis |
| 9 | 77 | 77.8 | 31 18 AAW17082 | Foot and mouth dis |

| | | | | |
|----|----|------|-----------------|---------------------|
| 10 | 77 | 77.8 | 35 21 AAY68501 | Target antigenic p |
| 11 | 77 | 77.8 | 75 21 AAY68528 | Synthetic foot and |
| 12 | 77 | 77.8 | 216 4 AAP30205 | Sequence encoded b |
| 13 | 77 | 77.8 | 220 4 AAP30195 | Sequence encoded b |
| 14 | 77 | 77.8 | 233 4 AAP30204 | Sequence encoded b |
| 15 | 77 | 77.8 | 405 4 AAP30203 | Sequence encoded b |
| 16 | 77 | 77.8 | 406 4 AAP30202 | Sequence encoded b |
| 17 | 77 | 77.8 | 609 4 AAP30206 | Sequence encoded b |
| 18 | 74 | 74.7 | 31 18 AAW17086 | Foot and mouth dis |
| 19 | 73 | 73.7 | 31 18 AAW17087 | Foot and mouth dis |
| 20 | 71 | 71.7 | 31 18 AAW17084 | Foot and mouth dis |
| 21 | 70 | 70.7 | 31 18 AAW17083 | Foot and mouth dis |
| 22 | 70 | 70.7 | 31 18 AAW17088 | Foot and mouth dis |
| 23 | 70 | 70.7 | 213 4 AAP30198 | Sequence encoded b |
| 24 | 70 | 70.7 | 233 4 AAP30209 | Sequence of antigen |
| 25 | 69 | 69.7 | 35 21 AAY68502 | Target antigenic p |
| 26 | 69 | 69.7 | 35 21 AAY68508 | Consensus antigen |
| 27 | 69 | 69.7 | 46 21 AAY68503 | Target antigenic p |
| 28 | 69 | 69.7 | 65 21 AAY68527 | Synthetic foot and |
| 29 | 69 | 69.7 | 75 21 AAY68529 | Synthetic foot and |
| 30 | 67 | 67.7 | 35 7 AAP60895 | peptide containing |
| 31 | 67 | 67.7 | 35 9 AAP82746 | VP1(A12,119) contg |
| 32 | 66 | 66.7 | 20 5 AAP40103 | Sequence at antigen |
| 33 | 66 | 66.7 | 216 5 AAP40085 | Sequence of foot a |
| 34 | 63 | 63.6 | 248 4 AAP30207 | Sequence of an FMD |
| 35 | 62 | 62.6 | 18 4 AAP30110 | Sequence of VP1 ca |
| 36 | 61 | 61.6 | 35 21 AAY68509 | Consensus antigen |
| 37 | 61 | 61.6 | 55 21 AAY68533 | Synthetic foot and |
| 38 | 57 | 57.6 | 218 4 AAP30196 | Sequence encoded b |
| 39 | 55 | 55.6 | 28 4 AAP30316 | Sequence of VP1 ca |
| 40 | 54 | 54.5 | 213 21 AAB15428 | FMDV antigen for r |
| 41 | 54 | 54.5 | 213 21 AAB15397 | Foot-and-mouth dis |
| 42 | 54 | 54.5 | 213 21 AAB15398 | Foot-and-mouth dis |
| 43 | 54 | 54.5 | 213 21 AAB15402 | Foot-and-mouth dis |
| 44 | 53 | 53.5 | 36 7 AAP60896 | peptide containing |
| 45 | 53 | 53.5 | 36 9 AAP82747 | VP1(A24,C) contg. |

ALIGNMENTS

| | |
|-------------------------------------|--|
| RESULT 1 | |
| AAAR38543 | |
| AAAR38543 standard; peptide: 20 AA. | |
| XX | |
| AC | AAAR38543; |
| XX | |
| DT | 25-MAR-2003 (updated) |
| DT | 11-JAN-1994 (first entry) |
| XX | |
| DE | Foot and Mouth Disease Virus VPI antigenic peptide. |
| XX | |
| KW | Multivalent vaccine; polyllysine; homopolymer; dendritic core; |
| KW | multiple antigen peptide system; MAPs; Foot and Mouth Disease; |
| KW | FMDV; VPI protein; Aphthovirus; vaccine. |
| XX | |
| OS | Foot and Mouth Disease Virus. |
| XX | |
| PM | US5229490-A. |
| XX | |
| PD | 20-JUL-1993. |
| XX | |
| PF | 20-DEC-1990; 90US-0631185. |
| XX | |
| PR | 06-MAY-1987; 87US-0047204. |
| PR | 30-JUN-1987; 87US-0068840. |
| PR | 12-APR-1989; 89US-0336845. |
| XX | 20-DEC-1990; 90US-0631185. |
| XX | |
| PA | (UYRO) UNIV ROCKEFELLER. |
| XX | |
| PI | Tam JP; |
| XX | |

DR WPI; 1993-242534/30.
 XX
 PT Multiple antigenic peptide systems - have dendritic core attached
 PT covalently to antigens, used as vaccine
 XX
 PS Claim 26; Column 24; 23pp; English.
 XX
 CC This is a preferred FMDV antigenic peptide suitable for
 CC construction of a Multiple Antigen Peptide System (MAPS) by
 CC covalent coupling to a dendritic homopolymer core (esp.
 CC polylysine). The antigen is derived from the Foot and Mouth Disease
 CC virus VP1 protein.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC
 SQ Sequence 20 AA;
 XX
 QY Query Match 90.9%; Score 90; DB 14; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Db 2 GSGVRGDSGSLARVARQL 20
 1 GSGVRGDSGSLARVARQL 19
 XX
 RESULT 2
 AAR41793
 ID AAR41793 standard; protein; 20 AA.
 XX
 AC AAR41793;
 XX
 DT 25-MAR-2003 (updated)
 DT 25-MAR-1994 (first entry)
 XX
 DE Foot and Mouth Disease Virus VPI antigen.
 XX
 XX Group A Streptococci; surface antigen; anchor region;
 KM gram positive bacterium; M protein; fusion protein; immunogen;
 KM FMDV VPI; vaccine.
 KM
 XX
 OS Foot and Mouth Disease Virus.
 OS
 PN WO9318163-A2.
 PN
 PD 16-SEP-1993.
 PD
 PF 12-MAR-1993; 93WO-US023355.
 PF
 PR 13-MAR-1992; 92US-0851082.
 PR
 PA (UYRQ) UNITV ROCKEFELLER.
 PA
 XX
 PI Fischetti VA, Pozzi G, Schneewind O;
 PI
 DR WPI; 1993-303477/38.
 DR
 PT Gene encoding hybrid surface protein of gram positive bacteria -
 PT useful for preparing vaccine compsn. for protecting animals from
 PT bacterial infection
 PT
 PS Disclosure; Page 55; 85pp; English.
 PS
 XX Hybrid surface proteins are claimed in which an active
 CC polypeptide (e.g. a surface antigen from a mammalian tumour cell,
 CC sperm or an allergen, bacterium, virus, parasite or fungus) is
 CC fused to an anchor region from a surface antigen normally expressed
 CC on the cell surface of gram positive bacteria. The anchor segment
 CC is pref. derived from a streptococcal M protein (see AAR41780).
 CC Sequence AAR41793 is a peptide sequence from the VPI protein of
 CC Foot and Mouth Disease virus (Nature 298:30 (1983)) suitable for
 CC development of a vaccine against FMDV.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX

SQ Sequence 20 AA;
 XX
 QY Query Match 90.9%; Score 90; DB 14; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Db 2 GSGVRGDSGSLARVARQL 20
 1 GSGVRGDSGSLARVARQL 19
 XX
 RESULT 3
 AAM17085
 ID AAM17085 standard; peptide; 31 AA.
 XX
 AC AAM17085;
 XX
 DT 13-JUN-1997 (first entry)
 DT
 XX
 DE Foot and mouth disease virus modified G-H loop of protein VP-1.
 XX
 KM Foot and mouth disease; aphthovirus; vaccine; antigen; epitope;
 KM Immunogen; G-H loop; VP-1; deletion; mutant; binding site removal;
 KM antibody; non-infectious; attenuated.
 KM
 XX
 OS Foot and mouth disease virus.
 OS
 XX
 XX Key Location/Qualifiers
 FH MISC-difference 18
 FT MISC-difference 18
 FT /label- substitution
 FT /note- "wild-type Phe replaced with Lys"
 FT MISC-difference 23
 FT /label- substitution
 FT /note- "wild-type Pro replaced with Leu"
 FT
 XX
 PN US5612040-A.
 PN
 PD 18-MAR-1997.
 PD
 PF 07-APR-1995; 95US-0418716.
 PF
 PR 07-APR-1995; 95US-0418716.
 PR
 PA (USDA) US SEC OF AGRIC.
 PA
 XX
 XX Baxt B, Berenstein A, Kang AS, Mason PW, Reider E;
 XX
 PI
 PI
 DR WPI; 1997-192081/17.
 DR
 PT Genetically modified foot-and-mouth disease virus - lacks
 PT cell-binding site and is non-infectious, useful in vaccines
 PT
 PS Disclosure; Figure 1; 10pp; English.
 PS
 XX AAM17083-W17088 are peptides representing mutant versions of amino acids
 CC 130-163 of wild-type foot and mouth disease (FMD) virus VP-1 structural
 CC protein. The mutants were made in order to investigate the requirements
 CC of this region for cell binding. The sequences are mutant versions of
 CC the G-H loop, a flexible loop between the G and H beta strands of VP-1)
 CC VP-1, which is the main antigenic site of VP-1 and is also involved in
 CC cell binding. The FMD virus G-H loop peptide can be modified in a FMD
 CC virus by deletion of the amino acid (aa) sequence
 CC Gly-Val-Arg-Gly-Asp-Phe (aa 142-147) and replacing this sequence with the
 CC sequence Asn-Pro. This results in the virus retaining its immunogenicity
 CC but is not infectious because the cell binding site has been removed. The
 CC genetically modified FMD virus is useful in vaccines against the
 CC disease.
 CC
 SQ Sequence 31 AA;
 XX
 QY Query Match 86.9%; Score 86; DB 18; Length 31;
 Best Local Similarity 94.7%; Pred. No. 6.7e-06;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX

QY 2 GSGVGDGSLALRVARQL 20
 ||||| |||||
 Db 11 GSGVGDGSLALRVARQL 29

RESULT 4
 AB008643
 ID AB008643 standard; peptide: 19 AA.
 XX
 AC AB008643;
 XX
 DT 04-JUN-2003 (first entry)
 XX
 DE Foot and mouth disease virus (FMDV) VP1-A12141-159, variant FL.
 XX
 KW Foot and mouth disease virus; FMDV; VP1-A12 region; immunosuppressive;
 KW antiinflammatory; antirheumatic; antirheumatic; dermatological;
 KW antidiabetic; antianaemic; neuroprotective; vaccine;
 KW anti-metallothionein antibody; humoral immune response;
 KW autoimmune disease; Grave's disease; rheumatoid arthritis;
 KW systemic lupus erythematosus; Type 1 diabetes; pernicious anaemia;
 KW multiple sclerosis; Sjorgen's disease.
 XX
 PA Foot and mouth disease virus.
 XX
 OS US2003007973-A1.
 XX
 PN 09-JAN-2003.
 XX
 PD 24-JUN-2002; 2002US-0178909.
 XX
 PF 22-JUN-2001; 2001US-300346P.
 XX
 PR (LYNE/) LYNES M A.
 XX
 PS Lyles MA;
 XX
 PI WPI: 2003-353082/33.
 XX
 DR WPI: 2003-353082/33.
 XX
 PS Treating autoimmune diseases, e.g. Grave's disease, arthritis, lupus,
 PT or diabetes by administering a composition consisting of an
 PT anti-metallothionein antibody to stimulate a humoral immune response in
 PT a subject -
 XX
 PS Example 7; Fig 9; 24pp; English.
 XX
 CC The invention describes a method of treating a subject comprising
 CC administering to the subject a composition consisting of an
 CC anti-metallothionein antibody to stimulate a humoral immune response in
 CC a subject. The methods and compositions are useful for treating
 CC autoimmune diseases, e.g. Grave's disease, rheumatoid arthritis,
 CC systemic lupus erythematosus, Type 1 diabetes, pernicious anaemia,
 CC multiple sclerosis or Sjorgen's disease. This is the amino acid
 CC sequence of foot and mouth disease virus (FMDV) VP1-A12141-159 region
 CC used as an immunogen.
 CC
 SQ Sequence 19 AA;
 XX

Query Match 84.8%; Score 84; DB 24; Length 19;
 Best Local Similarity 94.7%; Pred. No. 8.2e-06;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGVGDGSLALRVARQL 20
 ||||| |||||
 Db 1 GSGVGDGSLALRVARQL 19

RESULT 5
 AB008642
 ID AB008642 standard; peptide: 19 AA.
 XX
 AC AB008642;
 XX

XX 04-JUN-2003 (first entry)
 DT
 XX
 DE Foot and mouth disease virus (FMDV) VP1-A12141-159, variant FP.
 DE
 XX
 KW Foot and mouth disease virus; FMDV; VP1-A12 region; immunosuppressive;
 KW antiinflammatory; antirheumatic; antirheumatic; dermatological;
 KW antidiabetic; antianaemic; neuroprotective; vaccine;
 KW anti-metallothionein antibody; humoral immune response;
 KW autoimmune disease; Grave's disease; rheumatoid arthritis;
 KW systemic lupus erythematosus; Type 1 diabetes; pernicious anaemia;
 KW multiple sclerosis; Sjorgen's disease.
 XX
 PA Foot and mouth disease virus.
 XX
 OS US2003007973-A1.
 XX
 PN 09-JAN-2003.
 XX
 PD 24-JUN-2002; 2002US-0178909.
 XX
 PF 22-JUN-2001; 2001US-300346P.
 XX
 PR (LYNE/) LYNES M A.
 XX
 PS Lyles MA;
 XX
 PI WPI: 2003-353082/33.
 XX
 DR WPI: 2003-353082/33.
 XX
 PS Treating autoimmune diseases, e.g. Grave's disease, arthritis, lupus,
 PT or diabetes by administering a composition consisting of an
 PT anti-metallothionein antibody to stimulate a humoral immune response in
 PT a subject -
 XX
 PS Example 7; Fig 9; 24pp; English.
 XX
 CC The invention describes a method of treating a subject comprising
 CC administering to the subject a composition consisting of an
 CC anti-metallothionein antibody to stimulate a humoral immune response in
 CC a subject. The methods and compositions are useful for treating
 CC autoimmune diseases, e.g. Grave's disease, rheumatoid arthritis,
 CC systemic lupus erythematosus, Type 1 diabetes, pernicious anaemia,
 CC multiple sclerosis or Sjorgen's disease. This is the amino acid
 CC sequence of foot and mouth disease virus (FMDV) VP1-A12141-159 region
 CC used as an immunogen.
 CC
 SQ Sequence 19 AA;
 XX

Query Match 77.8%; Score 77; DB 24; Length 19;
 Best Local Similarity 89.5%; Pred. No. 9.2e-05;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSGVGDGSLALRVARQL 20
 ||||| |||||
 Db 1 GSGVGDGSLALRVARQL 19

RESULT 6
 AAY94587
 ID AAY94587 standard; peptide: 20 AA.
 XX
 AC AAY94587;
 XX
 DT 10-JAN-2001 (first entry)
 XX
 DE Envelope gene epitope of foot and mouth disease virus.
 XX
 KW Hepatitis B virus nucleocapsid antigen; HBcAg; T cell epitope;
 KW cytolytic T lymphocyte; immunogenic; ICG; CTL; FMDV;
 KW immunodominant core epitope; immunisation; envelope gene.
 XX
 OS Foot and mouth disease virus.
 XX

PN W0200026385-A1.
XX
PD 11-MAY-2000.
XX
PF 05-NOV-1999; 99WO-US26291.
XX
PR 05-NOV-1998; 98US-0107169.
XX
PA (POWD-) POWDERJECT VACCINES INC.
XX
PI Fuller DL, Fuller JT;
XX
DR WPI: 2000-451623/39.
XX
XX Use of expression vector for nucleic acid immunization that comprises
PT promoter and recombinant nucleic acid sequences encoding Hepatitis B
PT core antigen and T cell epitope from antigen -
XX
PS Example 6; Page 39; 55pp; English.
XX
XX The present invention relates to an immunogenetic recombinant
CC nucleic acid molecule. The molecule consists of a modified hepatitis
CC B virus nucleocapsid antigen (HBcAg) with a T cell epitope sequence
CC inserted within the HBcAg. The creation of a unique restriction site
CC in HBcAg facilitated the insertion of the T cell epitope into the DNA
CC encoding the immunodominant core epitope of the HBcAg. An example of a
CC suitable insertion epitope is the present sequence, the
CC gene. Alternatively other T cell epitopes may be inserted
CC (AAV94583, AAV94584, AAV94585, AAV94586, AAV94588). The recombinant
CC nucleic acid molecule may then be used as a reagent in various nucleic
CC acid immunisation strategies. The advantage of this method of
CC immunisation is that the nucleic acid reagents that encode hybrid HBcAg
CC generate an extremely high frequency cellular immune response against
CC the CTL epitope.
XX
SQ Sequence 20 AA;
XX
Query Match 77.8%; Score 77; DB 21; Length 20;
Best Local Similarity 89.5%; Pred. No. 9.7e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 GSGVGRGDSIALPRVARQL 20
Db 1 GSGVGRGDSIALPRVARQL 19
XX
RESULT 7
AAP30107
ID AAP30107 standard; Peptide: 31 AA.
XX
AC AAP30107;
XX
DT 03-APR-1992 (first entry)
XX
DE Sequence of VP1 capsid protein residues 130-160 from the amino-
DE terminus, FMDV, Tudinggen type A, subtype 12, strain 119.
XX
KM Antigen: Picornavirus; capsid protein; antibody; detection;
KM vaccine; diagnosis.
XX
OS Foot and mouth disease virus.
XX
XX
XX W08303547-A.
XX
PD 27-OCT-1983.
XX
PF 14-APR-1983; 83WO-0002644.
XX
PR 25-MAR-1983; 83US-0478847.
PR 14-APR-1982; 82US-0368308.
PR 20-SEP-1984; 84US-0653475.
PR 18-DEC-1984; 84US-0682819.

XX
PA (BITT/) BITTLE J L.
PA (SCRI-) SCRIPPS CLINIC & RE.
XX
PI Bittle JL, Lerner RA;
XX
DR WPI: 1983-807942/44.
XX
PT Antigenic peptide(s) corresp. to picornavirus capsid protein -
PT useful in prodn. of vaccines and in diagnostic tests
XX
PS Example; Page 26; 90pp; English.
XX
XX The peptides of the invention corresp. to a region on the antigenic
CC Picornavirus capsid protein. The capsid protein FMDV VP1 or polio
CC virus VP1. When linked to carriers the peptides are immunogenic.
CC Dose is 20 ug-2mg peptide for inoculations.
XX
SQ Sequence 31 AA;
XX

Query Match 77.8%; Score 77; DB 4; Length 31;
Best Local Similarity 89.5%; Pred. No. 0.00015;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 GSGVGRGDSIALPRVARQL 20
Db 11 GSGVGRGDSIALPRVARQL 29

RESULT 8
AAP50728
ID AAP50728 standard; protein; 31 AA.
XX
AC AAP50728;
XX
DT 23-OCT-1991 (first entry)
XX
DE Foot-and-mouth disease antigenic peptide.
XX
DE Foot-and-mouth disease; vaccine; antigen;
KM
XX
OS Foot-and-mouth disease virus.
XX
XX US4544500-A.
XX
PN 01-OCT-1985.
XX
PD 18-DEC-1984; 84US-0682819.
XX
PF 18-DEC-1984; 84US-0682819.
XX
PR 18-DEC-1984; 84US-0682819.
XX

(SCRI-) SCRIPPS CLINIC & RESEARCH FOUNDATION.

PI Bittle JL, Lerner RA;

DR WPI: 1985-262823/42.

PT Synthetic foot and mouth disease antigen - comprising 20 amino acid
PT peptide corresp. to virus protein VP1.
XX

PS Disclosure; page 4; 7pp; English.

XX The peptide corresponds to amino acids 130-160 of the foot and mouth
CC disease virus VP1 protein. It represents a monospecific synthetic
CC antigenic determinant. The peptide can be used to vaccinate animals,
CC esp. swine and cattle, against the virus with a single inoculation.
XX

SQ Sequence 31 AA;

Query Match 77.8%; Score 77; DB 6; Length 31;
Best Local Similarity 89.5%; Pred. No. 0.00015;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSGVRGDSGLAPVARQL 20
 ||||| |||||
 DB 11 GSGVRGDSGLAPVARQL 29

RESULT 9

AAW17082
 ID AAW17082 standard; peptide; 31 AA.

AAW17082;

13-JUN-1997 (first entry)

Foot and mouth disease virus G-H loop of protein VP-1.

KM Foot and mouth disease; aphthovirus; vaccine; antigen; epitope;
 immunogen; G-H loop; VP-1; deletion; mutant; binding site removal;
 KM antibody; non-infectious; attenuated.

Foot and mouth disease virus.

US5612040-A.

18-MAR-1997.

07-APR-1995; 95US-0418716.

07-APR-1995; 95US-0418716.

(USDA) US SEC OF AGRIC.

Bart B, Bernstein A, Kang AS, Mason PM, Reider E;

WPI; 1997-192081/17.

Genetically modified foot-and-mouth disease virus - lacks

cell-binding site and is non-infectious, useful in vaccines

disclosure; Figure 1; 10pp; English.

AAW17082 represents amino acids 130-163 of wild-type foot and mouth
 disease (FMD) virus VP-1 structural protein. The sequence represents
 the G-H loop, a flexible loop between the G and H beta strands of VP-1.
 The G-H loop is the main antigenic site of VP-1 and is also involved in
 cell binding. The FMD virus G-H loop peptide can be modified in a FMD
 virus by deletion of the amino acid (aa) sequence
 CC Gly-Val-Arg-Gly-Asp-Phe (aa 142-147) and replacing this sequence with the
 sequence Asp-Pro. This results in the virus retaining its immunogenicity
 CC but is not infectious because the cell binding site has been removed. The
 CC genetically modified FMD virus is useful in vaccines against the
 CC disease.

Sequence 31 AA;

Query Match 77.8%; Score 77; DB 18; Length 31;

Best Local Similarity 89.5%; Pred. No. 0.00015;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSGVRGDSGLAPVARQL 20
 ||||| ||||| |||||
 DB 11 GSGVRGDSGLAPVARQL 29

RESULT 10

AAV68501
 ID AAV68501 standard; peptide; 35 AA.

AAV68501;

05-MAY-2000 (first entry)

Target antigenic peptide derived from amino acids 134-169 of VP1.

KM Antigenic peptide; VP1 capsid protein; FMDV strain A12; epitope;
 KM helper T-cell epitope; immune response; vaccine; FMDV infection.
 XX
 XX

Foot and mouth disease virus.

WO966954-A1.

29-DEC-1999.

21-JUN-1999; 99WO-US13921.

20-JUN-1998; 98US-0106500.

(UNBI-) UNITED BIOMEDICAL INC.

Wang CY, Shen M;

WPI; 2000-160563/14.

Synthetic peptide used in protecting animals against Foot-and-Mouth
 Disease Virus infections comprises a helper T-cell epitope and a
 PT Foot-and-Mouth Disease Virus epitope conjugate -

Claim 1; Page 45; 115pp; English.

The present sequence represents a target antigenic peptide derived from
 CC the VP1 capsid protein of Foot and Mouth Disease Virus (FMDV) strain A12.
 CC The peptide is used to design synthetic epitopes, which are conjugated
 CC to a helper T-cell epitope and optionally an immunostimulator sequence.
 CC The peptides are covalently linked to each other, preferably by peptide
 CC bonds generated through direct synthesis. The synthetic vaccines of the
 CC invention require lower levels of biosecurity, have a reduced loss of
 CC immunogenic activity, are less prone to product instability and
 CC lot-to-lot variability and do not need periodic revision due to
 CC antigenic variation in the field. The peptides are used as immunogens
 CC in vaccines to generate an enhanced immune response against a FMDV
 CC antigen in animals, such as swine, cattle, sheep, goats and susceptible
 CC wild species. They can also be used to diagnose FMDV infection in a
 CC mammal.

Sequence 35 AA;

Query Match 77.8%; Score 77; DB 21; Length 35;

Best Local Similarity 89.5%; Pred. No. 0.00017;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSGVRGDSGLAPVARQL 20
 ||||| ||||| |||||
 DB 7 GSGVRGDSGLAPVARQL 25

RESULT 11

AAV68528
 ID AAV68528 standard; peptide; 75 AA.

AAV68528;

05-MAY-2000 (first entry)

Synthetic foot and mouth disease virus immunogen.

Antigenic peptide; VP1 capsid protein; serotype Asia; epitope;
 KM helper T-cell epitope; immune response; vaccine; FMDV infection.

Synthetic.

Yersinia sp.

Foot and mouth disease virus.

Key location/Qualifiers

Peptide 1..16 /note="Yersinia Invasin domain (immunostimulator
 FT Peptide 17..18 peptide"

| | |
|---|---|
| FT | /note= "spacer" |
| FT | 19..38 |
| FT | /note= "antologous helper T-cell epitope derived from VP1 capsid protein" |
| FT | Peptide |
| FT | 39..40 |
| FT | /note= "spacer" |
| FT | Peptide |
| FT | 41..75 |
| FT | /note= "synthetic VP1 capsid protein epitope" |
| PN | MO9966954-AI. |
| PD | |
| XX | 29-DEC-1999. |
| XX | |
| PF | 21-JUN-1999; 99WO-US13921. |
| XX | |
| PR | 20-JUN-1998; 98US-0100600. |
| XX | |
| PA | (UNBI-) UNITED BIOMEDICAL INC. |
| XX | |
| PI | Wang CY, Shen M; |
| XX | |
| DR | WPI: 2000-160563/14. |
| XX | |
| PT | Synthetic peptide used in protecting animals against Foot-and-Mouth Disease Virus infections comprises a helper T-cell epitope and a Foot-and-Mouth Disease Virus epitope conjugate - |
| PS | Claim 8; Page 96; 115pp; English. |
| CC | The present sequence represents a foot and mouth disease (FMDV) vaccine of the invention. The specification describes epitopes derived from an antigen of the VP1 capsid protein of FMDV. The VP1 epitopes are conjugated to a helper T-cell epitope and optionally an immunostimulator by peptide bonds generated through direct synthesis. The synthetic vaccines of the invention require lower levels of biosecurity, have a reduced loss of immunogenic activity, are less prone to product instability and lot-to-lot variability and do not need periodic revision due to antigenic variation in the field. The peptides are used as immunogens in vaccines to generate an enhanced immune response against a FMDV antigen in animals, such as swine, cattle, sheep, goats and susceptible wild species. They can also be used to diagnose FMDV infection in a mammal. |
| SO | Sequence 75 AA; |
| Query Match | 77.8%; Score 77; DB 21; Length 75; |
| Best Local Similarity | 89.5%; Pred. NO. 0.00037; |
| Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0; | |
| OY | 2 GSGVRGDSGLATRYAROL 20 |
| Db | 47 GSGVRGDFGSLAPRYAROL 65 |
| RESULT 12 | |
| AAP30205 | |
| AAP30205 standard; Protein: 216 AA. | |
| AAP30205; | |
| AC | |
| DT | 29-JUL-1992 (first entry) |
| XX | |
| DE | Sequence encoded by direct expression vector pFM 10 which comprises the promoter and operator of the E. coli cryptophan operon Aas 1-211 of the VP3 gene linked to 4 AAs from pBR322. |
| DE | |
| XX | |
| KM | Vaccine; immunogen; antigen; viral protein. |
| XX | |
| OS | Foot and mouth disease virus. |
| XX | |
| EP68693-A. | |

[illegible]

PS Disclosure; Fig 2; 81pp; English.

XX The inventors claim a polypeptide comprising at least one antigen of

CC FMDV, or a fusion polypeptide of at least two antigens from at least

CC two different FMDV strands, and encoding DNA. Pref. the fusion

CC polypeptide has the sequence of two of the A, C, O, Asia-1, SAT 1,

CC SAT 2 and SAT 3 type strains of the virus. The polypeptides pref.

CC comprise Aas 55-177 or 1-210 of the VP3 virus. Fusion polypeptides

CC may comprise Aas 1-210 fused to 8-210 of VP3 virus protein. pFM1,

CC pFM2, pFM3, pFM10, pFM20, pFM1, pFMC, pFMD, pFMF and pFMG are also

CC claimed.

XX

XX Sequence 220 AA;

SO

Query Match 77.8%; Score 77; DB 4; Length 220;

Best Local Similarity 89.5%; Pred. No. 0.0011;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSGVRGDSGLARVARQL 20

Db 140 GSGVRGDSGLARVARQL 158

RESULT 14

AAP30204

ID AAP30204 standard; Protein; 233 AA.

XX

XX AAP30204;

XX

XX 29-JUL-1992 (first entry)

XX

XX Sequence encoded by pFM3 which comprises 17 AAs from the LE' gene

DE construction (fragment 3a), linked to a methionine AA (CNR cleavable),

DE linked to the Aas 1-211 of the VP3 FMDV A12, linked to 4 AAs from

DE pBR322.

XX

XX Vaccine; immunogen; antigen; viral protein.

XX

XX Foot and mouth disease virus and Escherichia coli.

XX

XX EP68693-A.

XX

XX 05-JAN-1983.

XX

XX 11-JUN-1982; 82EP-0303040.

XX

XX 04-MAY-1982; 82US-0374855.

PR 16-JUN-1981; 81US-0274103.

XX

XX (GETH) GENENTECH INC.

XX

XX Kleid DG, Yansura DG;

XX

XX WPI: 1983-05055K/03.

DR N-PSDB; AAN30142.

XX

XX Polypeptide antigens of foot-and-mouth disease - obt'd. by

PT recombinant DNA technology for vaccine prodn.

XX

XX Example; Page 33-34; 81pp; English.

XX

XX The inventors claim a polypeptide comprising at least one antigen of

CC FMDV, or a fusion polypeptide of at least two antigens from at least

CC two different FMDV strands, and encoding DNA. Pref. the fusion

CC polypeptide has the sequence of two of the A, C, O, Asia-1, SAT 1,

CC SAT 2 and SAT 3 type strains of the virus. The polypeptides pref.

CC comprise Aas 55-177 or 1-210 of the VP3 virus. Fusion polypeptides

CC may comprise Aas 1-210 fused to 8-210 of VP3 virus protein. pFM1,

CC pFM2, pFM3, pFM10, pFM20, pFM1, pFMC, pFMD, pFMF and pFMG are also

CC claimed.

XX

XX Sequence 233 AA;

SO

Query Match 77.8%; Score 77; DB 4; Length 233;

Best Local Similarity 89.5%; Pred. No. 0.0012;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSGVRGDSGLARVARQL 20

Db 158 GSGVRGDSGLARVARQL 176

RESULT 15

AAP30202

ID AAP30202 standard; Protein; 405 AA.

XX

XX AAP30202;

XX

XX 29-JUL-1992 (first entry)

XX

XX Sequence encoded by pFM1 which comprises 190 AAs from the LE' gene

DE construction linked to 6 AAs from the linker molecule (fragment 4),

DE linked to 205 AAs from the VP3 FMDV A12 (codons 7-211), linked to

DE 4 AAs from pBR322.

XX

XX Vaccine; immunogen; antigen; viral protein.

XX

XX Foot and mouth disease virus and Escherichia coli.

XX

XX EP68693-A.

XX

XX 05-JAN-1983.

XX

XX 11-JUN-1982; 82EP-0303040.

XX

XX 04-MAY-1982; 82US-0374855.

PR 16-JUN-1981; 81US-0274103.

XX

XX (GETH) GENENTECH INC.

XX

XX Kleid DG, Yansura DG;

XX

XX WPI: 1983-05055K/03.

DR N-PSDB; AAN30140.

XX

XX Polypeptide antigens of foot-and-mouth disease - obt'd. by

PT recombinant DNA technology for vaccine prodn.

XX

XX Example; Page 29-31; 81pp; English.

XX

XX The inventors claim a polypeptide comprising at least one antigen of

CC FMDV, or a fusion polypeptide of at least two antigens from at least

CC two different FMDV strands, and encoding DNA. Pref. the fusion

CC polypeptide has the sequence of two of the A, C, O, Asia-1, SAT 1,

CC SAT 2 and SAT 3 type strains of the virus. The polypeptides pref.

CC comprise Aas 55-177 or 1-210 of the VP3 virus. Fusion polypeptides

CC may comprise Aas 1-210 fused to 8-210 of VP3 virus protein. pFM1,

CC pFM2, pFM3, pFM10, pFM20, pFM1, pFMC, pFMD, pFMF and pFMG are also

CC claimed.

XX

XX Sequence 405 AA;

SO

Query Match 77.8%; Score 77; DB 4; Length 405;

Best Local Similarity 89.5%; Pred. No. 0.002;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSGVRGDSGLARVARQL 20

Db 330 GSGVRGDSGLARVARQL 348

Search completed: October 9, 2003, 10:14:18

Job time : 58.333 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2003, 10:10:09 ; Search time 19.6667 Seconds

(without alignments)
97.799 Million cell updates/sec

Title: US-09-549-186b-9

Perfect score: 1 CCGGVRGDSGSLARVAROL 20

Sequence: 1 CCGGVRGDSGSLARVAROL 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR_76:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------|----------------------|
| 1 | 77.8 | 2332 | 1 | GNNY4F | genome polyprotein |
| 2 | 66.7 | 216 | 2 | A03911 | genome polyprotein |
| 3 | 50.5 | 76 | 2 | D82844 | carbon storage, reg |
| 4 | 50.5 | 170 | 2 | T35564 | ribosomal protein |
| 5 | 49.5 | 230 | 2 | A03909 | genome polyprotein |
| 6 | 48.5 | 2336 | 2 | S37077 | genome polyprotein |
| 7 | 46.5 | 134 | 2 | F72250 | ribosomal protein |
| 8 | 46.5 | 312 | 2 | A56911 | TRADP protein - hu |
| 9 | 46.5 | 2333 | 1 | GNNY2F | genome polyprotein |
| 10 | 45.5 | 398 | 2 | A58922 | esterase/N-deacetyl |
| 11 | 45.5 | 467 | 2 | B75322 | probable oligoendo |
| 12 | 45.5 | 512 | 2 | S06115 | alpha-amylase (EC |
| 13 | 44.4 | 109 | 2 | S61252 | genome polyprotein |
| 14 | 44.4 | 109 | 2 | S61253 | genome polyprotein |
| 15 | 44.4 | 136 | 2 | H90573 | ribosomal protein |
| 16 | 44.4 | 537 | 2 | AB1869 | type I site-specif |
| 17 | 43.4 | 122 | 2 | S72797 | probable K+ transp |
| 18 | 43.4 | 130 | 2 | E82669 | 30S ribosomal prot |
| 19 | 43.4 | 151 | 2 | H70976 | probable ribosomal |
| 20 | 43.4 | 153 | 2 | S72982 | ribosomal protein |
| 21 | 43.4 | 211 | 2 | T35272 | hypothetical prote |
| 22 | 43.4 | 281 | 1 | S34626 | translational elonga |
| 23 | 43.4 | 303 | 2 | E72463 | hypothetical prote |
| 24 | 43.4 | 372 | 2 | A11573 | MDPH-dependent bu |
| 25 | 43.4 | 439 | 2 | S73586 | probable lipoprote |
| 26 | 42.4 | 99 | 2 | F82709 | hypothetical prote |
| 27 | 42.4 | 239 | 2 | A61167 | corticotropin / li |
| 28 | 42.4 | 250 | 2 | H87257 | hypothetical prote |
| 29 | 42.4 | 326 | 2 | A99757 | homolog of Salmo |

| | | | | | | |
|----|----|------|------|---|--------|--------------------|
| 30 | 42 | 42.4 | 326 | 2 | G85620 | homolog of Salmo |
| 31 | 42 | 42.4 | 356 | 2 | D64834 | probable membrane |
| 32 | 42 | 42.4 | 372 | 2 | AF1220 | MDPH-dependent bu |
| 33 | 42 | 42.4 | 373 | 2 | T50605 | hypothetical prote |
| 34 | 42 | 42.4 | 439 | 2 | A45068 | 5'-3' DNA helicase |
| 35 | 42 | 42.4 | 500 | 1 | S60929 | probable aldehyde |
| 36 | 42 | 42.4 | 694 | 2 | T33561 | hypothetical prote |
| 37 | 42 | 42.4 | 809 | 1 | S60112 | transitional endop |
| 38 | 42 | 42.4 | 1015 | 1 | JS0628 | formate dehydrogen |
| 39 | 42 | 42.4 | 1015 | 2 | C85729 | hypothetical prote |
| 40 | 42 | 42.4 | 1015 | 2 | E90888 | hypothetical prote |
| 41 | 42 | 42.4 | 1062 | 2 | D96540 | hypothetical prote |
| 42 | 42 | 42.4 | 1159 | 2 | AH3088 | icmf (imported) - |
| 43 | 42 | 42.4 | 1159 | 2 | B98198 | hypothetical prote |
| 44 | 42 | 42.4 | 1318 | 2 | T39066 | hypothetical prote |
| 45 | 42 | 42.4 | 1446 | 2 | T13018 | hypothetical prote |

ALIGNMENTS

RESULT 1

GNNY4F genome polyprotein - foot-and-mouth disease virus A (strain A12)

N:Contains: coat protein VP1; coat protein VP2; coat protein VP3; coat protein VP4; C: tein VPg2; genome-linked protein VPg3; nonstructural protein p20a; proteinase (EC 3.4

C:Species: Aphthovirus A (foot-and-mouth disease virus A)

C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999

C:Accession: A25794

R:Robertson, B.H.; Grubman, M.J.; Weddell, G.N.; Moore, D.M.; Welsh, J.D.; Fischer, T

J. Virol. 54, 651-660, 1985

A:Title: Nucleotide sequence and amino acid sequence coding for polypeptides of foot-and-mouth

A:Reference number: A25794; PMID:85211015; PMID:2987518

A:Accession: A25794

A:Molecule type: genomic RNA

A:Residues: 1-2332 <ROB>

A:Cross-references: GB:M0975; NID:g210306; PIDN:AAA42593.1; PID:g210307

C:Superfamily: foot-and-mouth disease virus genome polyprotein

C:Keywords: coat protein; core protein; genome-linked protein; hydroxylase; nonstructur

F:1-216/Product: nonstructural protein p20a #status predicted <C14>

F:217-285/Product: coat protein VP4 #status predicted <VP4>

F:286-503/Product: coat protein VP2 #status predicted <VP2>

F:504-723/Product: coat protein VP3 #status predicted <VP3>

F:724-937/Product: coat protein VP1 #status predicted <VP1>

F:938-953/Product: core protein X #status predicted <CPX>

F:954-1107/Product: core protein p14 #status predicted <C14>

F:1108-1425/Product: core protein p41 #status predicted <C41>

F:1426-1578/Product: core protein p19 #status predicted <C19>

F:1579-1601/Product: genome-linked protein VPg1 #status predicted <VG1>

F:1602-1625/Product: genome-linked protein VPg2 #status predicted <VG2>

F:1626-1649/Product: genome-linked protein VPg3 #status predicted <VG3>

F:1650-1862/Product: proteinase #status predicted <PTS>

F:1863-2332/Product: RNA-directed RNA polymerase #status predicted <RRP>

Query Match 77.8%; Score 77; DB 1; Length 2332;

Best Local Similarity 89.5%; Pred. No. 0.002;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSGVRGDSGSLARVAROL 20
DB 864 GSGVRGDSGSLARVAROL 882

RESULT 2

A03911 genome polyprotein - foot-and-mouth disease virus A (strain A24 Cruzeiro) (fragment)

N:Contains: coat protein VP1; core protein p22

C:Species: Aphthovirus A (foot-and-mouth disease virus A)

C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 26-Aug-1999

C:Accession: A03911

R:McKoff, A.J.; Paynter, C.A.; Rowlands, D.J.; Boothroyd, J.C.

Nucleic Acids Res. 10, 8285-8295, 1982

A:Title: Comparison of the amino acid sequence of the major immunogen from three sero

A:Reference number: A37503; NCBI:83143292; PMID:6298715
A:Accession: A03911
A:Molecule type: genomic RNA
A:Residues: 1-216 <NA>
A:Cross-references: GB:02183; NID:g210312; PIDN:AAA42596.1; PID:g210313
C:Comment: Specific enzymatic cleavage in vivo yields mature proteins including coat protein
C:Superfamily: foot-and-mouth disease virus genome polypeptide
C:Keywords: polyprotein

Query Match 66.7%; Score 66; DB 2; Length 216;
Best Local Similarity 73.7%; Pred. No. 0.0089;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 GSGVRGDSGLALVAROL 20
DB 129 GSGVRGDSGLALVAROL 147

RESULT 3

D82844
Carbon storage regulator XRO125 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000

C:Accession: D82844

R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; NCBI:20355717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: D82844

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-76 <NA>

A:Cross-references: GB:AE003866; GB:AE003849; NID:g9104906; PIDN:AAF82938.1; GSPDB:GN001

A:Experimental source: strain 9a5c

R:Simposon, A.J.G.; Relnach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvares, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carver, H

as-Neto, E.; Docena, C.; El-Dorri, H.; Facinani, A.P.; Ferreira, A.J.S.

submitted to Genbank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeri, D.A

Rodrigues, V.; Rosa, A.J.; de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Teshahro, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XRO125

C:Superfamily: glycogen biosynthesis inhibitor

Query Match 50.5%; Score 50; DB 2; Length 76;
Best Local Similarity 81.8%; Pred. No. 0.94;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GSGVRGDSGS 11
DB 64 GSGVRGDSGS 74

RESULT 4

Ribosomal protein S9 - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 19-May-2000

C:Accession: T35564

R:Saunders, D.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, August 1998

A:Reference number: Z21583

A:Accession: T35564

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-170 <NA>
A:Cross-references: EMBL:AL031317; PIDN:CAA20391.1; GSPDB:GN00070; SCOEDB:SC6G4.13
A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: rps1; SCOEDB:SC6G4.13

C:Superfamily: Escherichia coli ribosomal protein S9

Query Match 50.5%; Score 50; DB 2; Length 170;
Best Local Similarity 57.9%; Pred. No. 2.1;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 GSGVRGDSGLALVAROL 20
DB 108 GSGVRGDSGLALVAROL 126

RESULT 5

A03909
genome polyprotein - foot-and-mouth disease virus A (strain A5) (fragment)

N:Contains: coat protein VP1; coat protein VP3; core protein p2

C:Species: Aphthovirus A (foot-and-mouth disease virus A)

C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 07-Feb-1997

C:Accession: A03909

R:Beck, E.; Fell, G.; Strohmaier, K.

EMBO J. 2, 555-559, 1983

A:Title: The molecular basis of the antigenic variation of foot-and-mouth disease vir

A:Reference number: A03909; NCBI:84028562; PMID:6194987

A:Accession: A03909

A:Molecule type: mRNA

A:Residues: 1-230 <NA>

A:Note: the authors translated the codon GCA for residue 114 as Val

C:Comment: Specific enzymatic cleavages in vivo yield mature proteins including the c

C:Superfamily: foot-and-mouth disease virus genome polypeptide

C:Keywords: polyprotein

Query Match 49.5%; Score 49; DB 2; Length 230;
Best Local Similarity 57.9%; Pred. No. 4.1;
Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 GSGVRGDSGLALVAROL 20
DB 143 GSGVRGDSGLALVAROL 161

RESULT 6

genome polyprotein - foot-and-mouth disease virus A (strain A22/550 Azerbaijan 65)

N:Contains: coat protein VP1; coat protein VP2; coat protein VP3; coat protein VP4; c

tein VPg2; Aphthovirus A (foot-and-mouth disease virus A)

C:Species: Aphthovirus A (foot-and-mouth disease virus A)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999

C:Accession: S37077; JN0413

R:Sosnovtsev, S.V.; Onischenko, A.M.; Petrov, N.A.; Kalashnikova, T.I.; Mamaeva, N.V.

submitted to the EMBL Data Library, August 1999

A:Reference number: S37077

A:Accession: S37077

A:Molecule type: genomic RNA

A:Residues: 1-2336 <SOS>

A:Cross-references: EMBL:X74812; NID:g397965; PIDN:CAA52812.1; PID:g397966

R:Onischenko, A.M.; Petrov, N.A.; Blinov, V.M.; Vassilenko, S.K.; Sandakhtchev, L.S.

Bioorg. Khim. 12, 416-419, 1986

A:Title: The DNA-copy primary structure for the gene of the FMDV A22 serotype VP1-pro

A:Reference number: JN0413; NCBI:86186952; PMID:2421736

A:Accession: JN0413

A:Molecule type: genomic RNA

A:Residues: 702-955 <ONP>

A:Cross-references: GB:M38362; NID:g210514; PIDN:AAA42664.1; PID:g210515

C:Superfamily: foot-and-mouth disease virus genome polypeptide

C:Keywords: coat protein; core protein; genome-linked protein; hydrolase; nonstructur

F:1-217/Product: nonstructural protein p20a #status predicted <NP>

F:218-286/Product: coat protein VP4 #status predicted <NP>

F:287-504/Product: coat protein VP2 #status predicted <NP>

F:505-724/Product: coat protein VP3 #status predicted <VP3>
 F:725-938/Product: coat protein VP1 #status predicted <VP1>
 F:939-954/Product: core protein X #status predicted <CPX>
 F:955-1108/Product: core protein p4 #status predicted <C41>
 F:1109-1426/Product: core protein p14 #status predicted <C14>
 F:1427-1579/Product: core protein p19 #status predicted <C19>
 F:1580-1602/Product: genome-linked protein VPg1 #status predicted <VG1>
 F:1603-1626/Product: genome-linked protein VPg2 #status predicted <VG2>
 F:1627-1650/Product: genome-linked protein VPg3 #status predicted <VG3>
 F:1651-1863/Product: proteinase #status predicted <PR>
 F:1864-2333/Product: RNA-directed RNA polymerase #status predicted <RR>

Query Match 48.5% Score 48; DB 2; Length 2336;
 Best Local Similarity 63.2%; Pred. No. 61;
 Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 2 GSGVRGDSGLARVARQL 20
 DB 865 GSGVRGDSGLARVARQL 883

RESULT 7
 F72250
 ribosomal protein S9 - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C:Accession: F72250
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.E.; Stewart, A.M.; Cotton, M.D.; Phillips, C.A.; Richardson, D.; C.M.

Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A:Reference number: A72200; MUID:99287316; PMID:10360571
 A:Accession: F72250
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1134 <ARN>
 A:Cross-references: GB:AE001797; GB:AE000512; NID:94982017; PIDN:AMD36521.1; PID:9498201
 A:Experimental source: strain MSB8
 C:Genetics:
 A:Gene: TM1453
 C:Superfamily: Escherichia coli ribosomal protein S9

Query Match 46.5% Score 46; DB 2; Length 134;
 Best Local Similarity 47.4%; Pred. No. 6.9;
 Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 2 GSGVRGDSGLARVARQL 20
 DB 73 GSGVRGDSGLARVARQL 91

RESULT 8
 A56911

TRAD protein - human
 N:Alternate names: TNF receptor 1-associated protein TRAD
 C:Species: Homo sapiens (hmn)
 C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 17-Mar-1999
 C:Accession: A56911
 R:Heu, H.; Xiong, J.; Goeddel, D.V.
 Cell 81, 495-504, 1995

A:Title: The TNF receptor 1-associated protein TRAD signals cell death and NF-kappaB ac
 A:Reference number: A56911; MUID:95277836; PMID:7758105
 A:Accession: A56911
 A>Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-312 <HSU>
 A:Cross-references: GB:L41690
 C:Genetics:
 A:Gene: GDB:TRAD
 A:Cross-references: GDB:1320395
 C:Keywords: apoptosis

Query Match 46.5% Score 46; DB 2; Length 312;
 Best Local Similarity 61.5%; Pred. No. 16;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 GSGVRGDSGLA 13
 DB 164 GSGVRGDSGLA 176

RESULT 9
 GNN2P

genome polypeptide - foot-and-mouth disease virus A (strain A[10]61)
 N:Contains: coat protein VP1; coat protein VP2; coat protein VP3; coat protein VP4; c
 protein p20a; nonstructural protein p20b; RNA-directed RNA polymerase (EC 2.7.7.48)
 C:Species: Aphthovirus A (foot-and-mouth disease virus A)
 C:Date: 17-Dec-1982 #sequence_revision 28-Aug-1985 #text_change 16-Jul-1999
 C:Accession: A93508; A91491; S30753
 R:Carroll, A.R.; Rowlands, D.J.; Clarke, B.E.
 Nucleic Acids Res. 12, 2461-2472, 1984

A:Title: The complete nucleotide sequence of the RNA coding for the primary translat
 A:Reference number: A93508; MUID:84169547; PMID:6324120
 A:Accession: A93508

A:Molecule type: genomic RNA
 A:Residues: 1-2333 <CAR>
 A:Cross-references: GB:X00429
 R:Boothroyd, J.C.; Harris, T.J.R.; Rowlands, D.J.; Lowe, P.A.
 Gene 17, 153-161, 1982

A:Title: The nucleotide sequence of cDNA coding for the structural proteins of foot-a
 A:Reference number: A91491; MUID:82211814; PMID:6282711
 A:Accession: A91491

A:Molecule type: genomic RNA
 A:Residues: 115-395, 'C', 397-631, 'L', 633-1048 <BOO>
 A:Cross-references: GB:V01130; NID:961048; PIDN:CAA24361.1; PID:91335402
 R:Sanger, D.V.; Newton, S.E.; Rowlands, D.J.; Clarke, B.E.

Nucleic Acids Res. 15, 3305-3315, 1987
 A:Title: All foot and mouth disease virus serotypes initiate protein synthesis at two
 A:Reference number: S30753; MUID:87203363; PMID:3033601
 A:Accession: S30753

A:Molecule type: genomic RNA

A:Cross-references: EMBL:M31575; NID:9210486; PIDN:AAA2655.1; PID:9210487
 C:Superfamily: foot-and-mouth disease virus genome polypeptide
 C:Keywords: coat protein; core protein; genome-linked protein; nonstructural protein;
 F:1-204/Product: nonstructural protein p20a #status predicted <NPA>
 F:205-286/Product: coat protein VP4 #status predicted <VP4>
 F:287-504/Product: coat protein VP2 #status predicted <VP2>
 F:505-725/Product: coat protein VP3 #status predicted <VP3>
 F:726-937/Product: coat protein VP1 #status predicted <VP1>
 F:938-1578/Product: core protein p52 #status predicted <CPP>
 F:1579-1601/Product: genome-linked protein VPg1 #status predicted <GL1>
 F:1602-1625/Product: genome-linked protein VPg2 #status predicted <GL2>
 F:1626-1649/Product: genome-linked protein VPg3 #status predicted <GL3>
 F:1650-1863/Product: nonstructural protein p20b #status predicted <NPB>
 F:1864-2333/Product: RNA-directed RNA polymerase #status predicted <RRP>

Query Match 46.5% Score 46; DB 1; Length 2333;
 Best Local Similarity 71.4%; Pred. No. 1.2e+02;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 7 GDSGLARVARQL 20
 DB 869 GDSGLARVARQL 882

RESULT 10

A58922
 esterase/N-deacetylase (EC 3.5.1.-), 50K hepatic - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 05-Dec-1998
 C:Accession: A58922
 R:Ozols, J.

submitted to the Protein Sequence Database, December 1998
 A:Description: Determination of Lumenal Orientation of Microsomal 50-kDa Esterase/N-D

A:Reference number: A58922
A:Accession: A58922
A:Molecule type: protein
A:Residues: 1-398 <OZO>
A:Experimental source: Oryctolagus cuniculus GV
C:Keywords: hydrolase

Query Match 45.5%; Score 45; DB 2; Length 398;
Best Local Similarity 63.2%; Pred. No. 30;
Matches 12; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 4 GVRGDS--GSLARVAROL 20
DB 183 GVSQDSAGNMLAAVAQQL 201

RESULT 11
B75322
probable oligonucleotidase F - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: B75322

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MID:20036896; PMID:10567266

A:Accession: B75322

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1467 <MHI>

A:Cross-references: GB:AE002041; GB:AE000513; NID:g6459838; PIDN:AAF11604.1; PID:g645984

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR2055

A:Map position: 1

Query Match 45.5%; Score 45; DB 2; Length 467;
Best Local Similarity 53.3%; Pred. No. 35;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGSGVRGDSGLALR 15
DB 103 CMNGVAGESTLARR 117

RESULT 12
S06115
alpha-amylase (EC 3.2.1.1) AMY1 precursor - yeast (Schwanniomyces occidentalis)

C:Species: Schwanniomyces occidentalis
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 22-Jun-1999
C:Accession: S06115

R:Strasser, A.W.M.; Selk, R.; Dolmen, R.J.; Niermann, T.; Bielefeld, M.; Seeboth, P.; Tu

Eur. J. Biochem. 184, 699-706, 1989

A:Title: Analysis of the alpha-amylase gene of Schwanniomyces occidentalis and the secre

A:Reference number: S06115; MID:90032659; PMID:2806251

A:Accession: S06115

A:Molecule type: DNA

A:Residues: 1-512 <STR>

C:Genetics:

A:Gene: AMY1

C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A:Pathway: glycogen/starch degradation

C:Superfamily: Aspergillus alpha-amylase: alpha-amylase core homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-25/Domain: signal sequence #status predicted <Sig>
F:26-512/Product: alpha-amylase #status predicted <MAT>
F:209-336/Domain: alpha-amylase core homology <AMT>

Query Match 45.5%; Score 45; DB 2; Length 512;

Best Local Similarity 47.1%; Pred. No. 38;
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 CGSGVRGDSGLALRVA 17
DB 475 CNSVLADSGSLSVSIS 491

RESULT 13
S61252
genome polypeptide - foot-and-mouth disease virus Asia (isolate Asia I Mandya, Karnat

N:Alternate names: immunogenic polypeptide
C:Species: Aphthovirus Asia (foot-and-mouth disease virus Asia)
A:Variety: isolate Asia I Mandya, Karnataka

C:Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 26-Aug-1999

C:Accession: S61252

R:Tulasiram, P.; Tyagi, M.; Suryanarayana, V.

submitted to the EMBL Data Library, June 1995

A:Description: Antigenic variation in foot and mouth disease virus type Asia I isolat

A:Reference number: S61252

A:Accession: S61252

A:Molecule type: mRNA

A:Residues: 1-109 <TUL>

A:Cross-references: EMBL:X88856; NID:g971407; PIDN:CAA61326.1; PID:g971408

A:Experimental source: isolate Asia I Mandya, Karnataka

C:Superfamily: foot-and-mouth disease virus genome polypeptide

C:Keywords: coat protein; polypeptide; proteinase

F:1-91/Product: coat protein VP1 (fragment) #status predicted <MAT>

F:92-107/Product: proteinase 2A #status predicted <MAT>

F:108-109/Product: proteinase 2B (fragment) #status predicted <MAT>

Query Match 44.4%; Score 44; DB 2; Length 109;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 RGDGSLARVAROL 20
DB 23 RGDMAALQRLSRQL 37

RESULT 14
S61253
genome polypeptide - foot-and-mouth disease virus Asia (isolate Asia I Nilgiri, Tamil

N:Alternate names: immunogenic polypeptide
C:Species: Aphthovirus Asia (foot-and-mouth disease virus Asia)
A:Variety: isolate Asia I Nilgiri, Tamil Nadu

C:Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 26-Aug-1999

C:Accession: S61253

R:Tulasiram, P.; Tyagi, M.; Suryanarayana, V.

submitted to the EMBL Data Library, June 1995

A:Description: Antigenic variation in foot and mouth disease virus type Asia I isolat

A:Reference number: S61253

A:Accession: S61253

A:Molecule type: mRNA

A:Residues: 1-109 <TUL>

A:Cross-references: EMBL:X88857; NID:g971409; PIDN:CAA61327.1; PID:g971410

A:Experimental source: isolate Asia I Nilgiri, Tamil Nadu

C:Superfamily: foot-and-mouth disease virus genome polypeptide
C:Keywords: coat protein; polypeptide; proteinase
F:1-91/Product: coat protein VP1 (fragment) #status predicted <MAT>
F:92-107/Product: proteinase 2A #status predicted <MAT>
F:108-109/Product: proteinase 2B (fragment) #status predicted <MAT>

Query Match 44.4%; Score 44; DB 2; Length 109;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

RESULT 15

H90573
ribosomal protein S9 [similarity] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-May-2002
C:Accession: H90573
R:Chambaud, I.; Heallig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallsen, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: H90573
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-136 <KUN>
A:Cross-references: GB:AL445566; PID:G1408910; PINN:CAC13669.1; GSPDB:GN00153
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYP4_4960
A:Genetic code: SGC3
C:Superfamily: Escherichia coli ribosomal protein S9

| | | | | |
|-------------|--------|--------------|------|--------------|
| Query Match | 44.48% | Score 44 | DB 2 | Length 136 |
| Best Local | 42.18% | Pred. No. 14 | | |
| Matches | 8 | Conservative | 5 | Mismatches 6 |
| | | | | Indels 0 |
| | | | | Gaps 0 |

```
QY      2 GSGVRGDSGLALRVARQL 20
        | | : | : | : | | |
Db      75 GCGLAGQAGAIRLGIARAL 93
```

Search completed: October 9, 2003, 10:18:44
Job time : 21.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 10:02:54 ; Search time 10.3333 Seconds

(without alignments)
91.019 Million cell updates/sec

Title: US-09-549-186b-9

Perfect score: 99

Sequence: 1 CGSGVRCGSGSLALRVARQL 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|------------------------------|
| 1 | 77.8 | 2332 | 1 | POLG_FMDVA | P03308 f genome po |
| 2 | 66.7 | 216 | 1 | POLG_FMDYC | P03309 foot-and-mo |
| 3 | 50.5 | 170 | 1 | RS9_STRCO | O53875 streptomyc |
| 4 | 49.5 | 129 | 1 | RS9_CHLYE | O88bk5 chlorobium |
| 5 | 49.5 | 230 | 1 | POLG_FMDV5 | P03307 foot-and-mo |
| 6 | 48.5 | 236 | 1 | POLG_FMDV5 | P03307 f genome po |
| 7 | 46.5 | 134 | 1 | RS9_THEMA | O91944 thermotoga |
| 8 | 46.5 | 312 | 1 | TRAD_HUMAN | O15628 homo sapien |
| 9 | 46.5 | 2333 | 1 | POLG_FMDV1 | P03306 f genome po |
| 10 | 45.5 | 501 | 1 | AMPA_BUCBP | O89ag2 buchnera ap |
| 11 | 45.5 | 512 | 1 | AMY1_DEBOC | P19269 debaryomyce |
| 12 | 44.4 | 94 | 1 | CH10_RHOHA | P23969 rhodospirillum rubrum |
| 13 | 44.4 | 95 | 1 | CH10_RHOHA | O91944 thermotoga |
| 14 | 44.4 | 128 | 1 | RR9_CYACA | O91944 thermotoga |
| 15 | 44.4 | 136 | 1 | RS9_MYCPU | O58q72 mycoplasma |
| 16 | 44.4 | 833 | 1 | SRC2_MOUSE | P32222 mus musculu |
| 17 | 43.4 | 110 | 1 | INS_PSAOB | O62587 psammomyces |
| 18 | 43.4 | 130 | 1 | RS9_XANAC | O89q41 xanthomonas |
| 19 | 43.4 | 130 | 1 | RS9_XANCP | O89q41 xanthomonas |
| 20 | 43.4 | 130 | 1 | RS9_XYUFA | O89q41 xanthomonas |
| 21 | 43.4 | 151 | 1 | RS9_MYCPU | O58q72 mycoplasma |
| 22 | 43.4 | 153 | 1 | RS9_MYCPU | O58q72 mycoplasma |
| 23 | 43.4 | 181 | 1 | EF1D_HUMAN | P23692 homo sapien |
| 24 | 43.4 | 348 | 1 | ADH1_PICST | O00097 picchia stip |
| 25 | 43.4 | 439 | 1 | YF82_MYCPN | P55585 rhizobium s |
| 26 | 43.4 | 516 | 1 | YF82_MYCPN | P55585 rhizobium s |
| 27 | 42.4 | 356 | 1 | YF82_MYCPN | P55585 rhizobium s |
| 28 | 42.4 | 439 | 1 | YF82_MYCPN | P55585 rhizobium s |
| 29 | 42.4 | 499 | 1 | YF82_MYCPN | P55585 rhizobium s |
| 30 | 42.4 | 809 | 1 | YF82_MYCPN | P55585 rhizobium s |
| 31 | 42.4 | 1015 | 1 | YF82_MYCPN | P55585 rhizobium s |
| 32 | 42.4 | 1318 | 1 | YF82_MYCPN | P55585 rhizobium s |
| 33 | 42.4 | 1355 | 1 | YF82_MYCPN | P55585 rhizobium s |

| | | | | | | |
|----|----|------|------|---|------------|--------------------|
| 34 | 41 | 41.4 | 108 | 1 | INS1_MOUSE | P01325 mus musculu |
| 35 | 41 | 41.4 | 195 | 1 | RERB_ARATH | O48671 arabidopsis |
| 36 | 41 | 41.4 | 271 | 1 | YMA8_MYCTU | O10526 mycobacteri |
| 37 | 41 | 41.4 | 306 | 1 | PYRD_METJA | O58070 methanococc |
| 38 | 41 | 41.4 | 449 | 1 | PCOL_HUMAN | O51113 homo sapien |
| 39 | 41 | 41.4 | 485 | 1 | MKR4_HUMAN | O13434 homo sapien |
| 40 | 41 | 41.4 | 759 | 1 | CI02_MOUSE | O92351 mus musculu |
| 41 | 41 | 41.4 | 914 | 1 | WA22_MYCTU | O06794 mycobacteri |
| 42 | 41 | 41.4 | 1004 | 1 | ATU2_YEAST | P38995 saccharomyc |
| 43 | 40 | 40.4 | 110 | 1 | INS1_RAT | P01322 rattus norv |
| 44 | 40 | 40.4 | 130 | 1 | RS9_LACLA | O9cdg7 lactococcus |
| 45 | 40 | 40.4 | 138 | 1 | RS9_ANASP | O8ypk7 anabaena sp |

ALIGNMENTS

RESULT 1
POLG_FMDVA STANDARD; PRT; 2332 AA.
AC P03308; P03312; Q65038; Q65039; Q65040; Q65041; Q65042; Q65043;
AC Q65044; Q65045; Q65046; Q65047;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 05, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Genome Polyprotein [Contains: Nonstructural protein P20A; Coat
DE Proteins VP1 TO VP4; Core proteins X, P14, P41, P19; Genome-linked
DE Proteins VP3 TO VP3; Picornavirus 3C (EC 3.4.22.28) (Protease 3C)
DE (P3C); RNA-directed RNA polymerase (EC 2.7.7.48)]
OS Foot-and-mouth disease virus (strain A12) (Aphthovirus A) (FMDV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12114;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85211015; PubMed=2987518;
RA Robertson B.H., Grubman M.J., Weddell G.N., Moore D.M., Welsh J.D.,
RA Fischer T., Dowbenko D.J., Yansura D.G., Small B., Kleid D.G.;
RT "Nucleotide and amino acid sequence coding for polypeptides of
RT foot-and-mouth disease virus type A12."
RT J. Virol. 54:651-660(1985).
RN [2]
RP SEQUENCE OF 1863-2332 FROM N.A.
RX MEDLINE=83225613; PubMed=6305004;
RA Robertson B.H., Morgan D.O., Moore D.M., Grubman M.J., Card J.,
RA Fischer T., Weddell G.N., Dowbenko D.J., Yansura D.G.;
RT "Identification of amino acid and nucleotide sequence of the
RT foot-and-mouth disease virus RNA polymerase."
RT Virology 126:614-623(1983).
RN [3]
RP SEQUENCE OF 715-955 FROM N.A.
RX MEDLINE=82061853; PubMed=6272395;
RA Kleid D.G., Yansura D.G., Small B., Dowbenko D.J., Moore D.M.,
RA Grubman M.J., Kerecner P.D., Morgan D.O., Robertson B.H.,
RA Bachrach H.L.;
RT "Cloned viral protein vaccine for foot-and-mouth disease: responses
RT in cattle and swine."
RT Science 214:1125-1129(1981).
RN [4]
RP CATALYTIC ACTIVITY: selective cleavage of Gln-|-Gly bond in the
RN poliovirus polyprotein. In other picornavirus reactions Glu may be
RN substituted for Gln, and Ser or Thr for Gly.
RN [5]
RP CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
RN {RNA} (N).
RN [6]
RP SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAEDRAL UNITS,
RN EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
RN VP3, AND VP4.
RN [7]
RP SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
RN [8]
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 DR EMBL: M10975; AAA42593.1; -;
 DR EMBL: J02187; AAA42670.1; -;
 DR MEROPS: C03.008.000.000;
 DR InterPro: IPR004004; Calic1_pol_hel.
 DR InterPro: IPR004080; FMDVp1coat.
 DR InterPro: IPR001676; Rhv.
 DR InterPro: IPR000605; RNA_helicase.
 DR InterPro: IPR007095; RNA_pol_DS_PS.
 DR InterPro: IPR001205; RNA_pol_P3D.
 DR InterPro: IPR007094; RNA_pol_PSV1r.
 DR Pfam: PF00073; rhv; 3.
 DR Pfam: PF00680; RNA_dep_RNA_pol; 1.
 DR Pfam: PF00910; RNA_helicase; 1.
 DR PRINTS: PR00918; CALICIVIRUS.
 DR PRINTS: PR01542; FMDVp1COAT.
 KW Polyprotein; Coat protein; Core protein; RNA-directed RNA polymerase;
 KW Transferase; Hydrolase; Thiol protease; Nonstructural protein;
 KW Myristate.

| FT CHAIN | 1 | 200 | NONSTRUCTURAL PROTEIN P20A. |
|-------------|----------|------------|------------------------------|
| FT CHAIN | 201 | 285 | COAT PROTEIN VP4. |
| FT CHAIN | 286 | 503 | COAT PROTEIN VP2. |
| FT CHAIN | 504 | 723 | COAT PROTEIN VP3. |
| FT CHAIN | 724 | 937 | COAT PROTEIN VP1. |
| FT CHAIN | 938 | 953 | CORE PROTEIN X. |
| FT CHAIN | 954 | 1107 | CORE PROTEIN P14. |
| FT CHAIN | 1108 | 1425 | CORE PROTEIN P41. |
| FT CHAIN | 1426 | 1578 | CORE PROTEIN P19. |
| FT CHAIN | 1579 | 1601 | GENOME-LINKED PROTEIN VP61. |
| FT CHAIN | 1602 | 1625 | GENOME-LINKED PROTEIN VP62. |
| FT CHAIN | 1626 | 1649 | GENOME-LINKED PROTEIN VP63. |
| FT CHAIN | 1650 | 1862 | PROTEASE. |
| FT CHAIN | 1863 | 2332 | RNA-DIRECTED RNA POLYMERASE. |
| FT LIPID | 201 | 201 | MYRISTATE. |
| SO SEQUENCE | 2332 AA; | 259408 MM; | EE77DA739CBEC6A CRC64; |

Query Match 77.8%; Score 77; DB 1; Length 2332;
 Best Local Similarity 89.5%; Pred. No. 0.002;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSGVRDGSGLARVARQL 20
 DB 864 GSGVRDGSGLARVARQL 882

 RESULT 2
 POLG_FMDV STANDARD; PRT; 216 AA.
 AC P03309;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Genome polyprotein [contains: Coat protein VP1; Core protein P52]
 DE (Fragment).
 OS Foot-and-mouth disease virus (strain A24 Cruzeiro) (Aphthovirus A)
 OS (FMDV).
 OS Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
 OC Aphthovirus.
 NC NCB1_TaxID=12115;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=83143292; PubMed=6298715;
 RA Makoff A.J., Paynter C.A., Rowlands D.J., Boothroyd J.C.;
 RT "Comparison of the amino acid sequence of the major immunogen from
 RT three serotypes of foot and mouth disease virus.";
 RL Nucleic Acids Res. 10:8285-8295(1982).
 CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
 CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
 CC VP3, AND VP4.
 CC -1- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.

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 DR EMBL: J02183; AAA42596.1; -;
 DR EMBL: A06733; CA00589.1; -;
 DR PTR: A03911; A03911.
 DR HSSP: Q88571; 1TME.
 DR InterPro: IPR004080; FMDVp1coat.
 DR InterPro: IPR001676; Rhv.
 DR Pfam: PF00073; rhv; 1.
 DR PRINTS: PR01542; FMDVp1COAT.
 KW Coat protein; Core protein; Polyprotein.
 FT NON_TER 1 1
 FT CHAIN 1 202 COAT PROTEIN VP1.
 FT CHAIN 203 >216 CORE PROTEIN P52.
 FT NON_TER 216 216
 SO SEQUENCE 216 AA; 23889 MM; 501659FF031A1D85 CRC64;

Query Match 66.7%; Score 66; DB 1; Length 216;
 Best Local Similarity 73.7%; Pred. No. 0.008;
 Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 GSGVRDGSGLARVARQL 20
 DB 129 GSGVRDGSGLARVARQL 147

 RESULT 3
 RS9_STRCO STANDARD; PRT; 170 AA.
 ID RS9_STRCO
 AC Q53875;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 30S ribosomal protein S9.
 GN RPS1 OR SC04735 OR SC664.13.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomyces.
 NC NCB1_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA MEDLINE=98102746; PubMed=9439573;
 RA Sanchez C., Blanco G., Mendez C., Salas J.A.;
 RT "Cloning, sequencing and transcriptional analysis of a Streptomyces
 RT coelicolor operon containing the rplM and rps1 genes encoding
 RL ribosomal proteins Scoli3 and Scos9.";
 RL Mol. Gen. Genet. 257:91-96(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdeno-Farraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinovitch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 CC -1- SIMILARITY: BELONGS TO THE S9P FAMILY OF RIBOSOMAL PROTEINS.

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DR EMBL; U43429; AAC46061.1; -
DR EMBL; AL939121; CAA20391.1; -
DR PIR; T35564; T35564.
DR HAMAP; MF_00532; -; 1.
DR InterPro; IPR000754; Ribosomal_S9.
DR Pfam; PF00380; Ribosomal_S9; 1.
DR ProDom; PD001627; Ribosomal_S9; 1.
DR PROSITE; PS00360; RIBOSOMAL_S9; 1.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 170 AA; 18699 MW; 3CEB0FF69151C99 CRC64;

Query Match 50.5%; Score 50; DB 1; Length 170;
Best Local Similarity 57.9%; Pred. No. 1.5;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 2 GSGVGDGSGSLARVAROL 20
DB 108 GGGVSGGAGLRLGVARAL 126

RESULT 4
RS9_CHLITE STANDARD; PRT; 129 AA.
ID RS9_CHLITE
AC O8BK85;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S9.
GN RPS1 OR C11782.
OS Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium.
OX NCBI_TaxID=1097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TLS / ATCC 49652 / DSM 12025;
RA EMBL; V01135; CAA24365.1; ALT_INIT.
RA MEDLINE; 22103685; PubMed=12093901;
RA Eelsen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
RA Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,
RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
RA Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,
RA Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;
RT "The complete genome sequence of Chlorobium tepidum TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium.";
RL Proc Natl Acad Sci U S A. 99:9509-9514(2002).
RL -1- SIMILARITY: BELONGS TO THE S9P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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DR EMBL; AE012931; AAM73003.1; -
DR TIGR; CT1782; -; 1.
DR HAMAP; MF_00532; -; 1.
DR InterPro; IPR000754; Ribosomal_S9.
DR Pfam; PF00380; Ribosomal_S9; 1.
DR ProDom; PD001627; Ribosomal_S9; 1.
DR PROSITE; PS00360; RIBOSOMAL_S9; 1.
KW Ribosomal protein; Complete proteome.

SQ SEQUENCE 129 AA; 14541 MW; D110858BA87B9BAC CRC64;

Query Match 49.5%; Score 49; DB 1; Length 129;
Best Local Similarity 47.4%; Pred. No. 1.6;
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 2 GSGVGDGSGSLARVAROL 20
DB 68 GGGLTGGGAVSLARAL 86

RESULT 5
POLG_FMDV5 STANDARD; PRT; 230 AA.
ID POLG_FMDV5
AC P03307;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Genome polyprotein [Contains: Coat proteins VP3, VP1, Core protein
DE P52] (fragment).
OS Foot-and-mouth disease virus (strain A5) (Aphthovirus A) (FMDV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12113;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84028562; PubMed=6194987;
RA Beck E., Feil G., Strohmaier K.;
RT "The molecular basis of the antigenic variation of foot-and-mouth
RT disease virus.";
RL EMBL J. 2:555-559(1983).
RL -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS,
CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC VP3, AND VP4.
CC -1- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC -----
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DR EMBL; V01135; CAA24365.1; ALT_INIT.
DR EMBL; V01135; CAA24366.1; ALT_SEQ.
DR PIR; A03909; A03909.
DR HSPD; O88571; 1TME.
DR InterPro; IPR004080; FMDV1coat.
DR InterPro; IPR001676; RVV.
DR Pfam; PF00073; RVV; 1.
DR PRINTS; PR01542; FMDV1COAT.
KW Coat protein; Core protein; Polypeptide.
FT NON_TER 1 1
FT CHAIN <1 4 COAT PROTEIN VP3.
FT CHAIN 5 216 COAT PROTEIN VP1.
FT CHAIN 217 >230 CORE PROTEIN P52.
FT NON_TER 230 230
SQ SEQUENCE 230 AA; 25369 MW; EA93A190F4CC1608 CRC64;

Query Match 49.5%; Score 49; DB 1; Length 230;
Best Local Similarity 57.9%; Pred. No. 2.9;
Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 2 GSGVGDGSGSLARVAROL 20
DB 143 GGGVGDGSGSAAARAKOL 161

RESULT 6
POLG_FMDVZ STANDARD; PRT; 2336 AA.
ID POLG_FMDVZ
AC P49303;

DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Genome polypeptide [Contains: Nonstructural protein P20A: Coat
DE proteins VP1 to VP4: Core proteins X, P14, P41, P19: Genome-linked
DE proteins VP1 to VP3: Picornain 3C (EC 3.4.22.28) (Protease 3C)
DE (33C): RNA-directed RNA polymerase (EC 2.7.7.48)]
OS Foot-and-mouth disease virus (strain A22/550 Azerbaijan 65)
OS (Aphthovirus A) (FMDV)
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_Taxid=73481;
RN [1]
RP SEQUENCE FROM N.A.
RA Sosnovtsev S.V., Onischenko A.M., Petrov N.A., Kalashnikova T.I.,
RA Mamaeva N.V., Dygin V.Y., Perevozchikova N.A., Vasilenco S.K.;
RL Submitted (Aug-1993) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Selective cleavage of Gln-I-gly bond in the
CC poliovirus polypeptide. In other picornavirus reactions Gln may be
CC substituted for Gln, and Ser or Thr for Gly.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate +
CC (RNA)(N).
CC -1- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHERAL UNITS,
CC EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2,
CC VP3, AND VP4.
CC -1- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
CC -----
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CC -----
DR EMBL: X74813; CAAS2812.1; -
DR PIR: S37077; S37077.
DR HSRP: Q88571; 1TME.
DR MEROPS: C03.008; -
DR InterPro: IPR004004; Calic1_pol_hel.
DR InterPro: IPR004080; FMDV1coat.
DR InterPro: IPR001676; Rbv.
DR InterPro: IPR000605; RNA_helicase.
DR InterPro: IPR007095; RNA_pol_DS_PS.
DR InterPro: IPR001205; RNA_pol_P3D.
DR InterPro: IPR007094; RNA_pol_PSV1r.
DR Pfam: PF00073; rhv. 3.
DR Pfam: PF00680; RNA_dep_RNA_pol. 1.
DR Pfam: PF00910; RNA_helicase. 1.
DR PRINTS: PR00918; CALICVIRUSNS.
DR PRINTS: PR01542; FMDV1COAT.
KW Polypeptide; Coat protein; Core protein; RNA-directed RNA polymerase;
KW Transferrase; Hydrolyase; Thiol protease; Nonstructural protein;
KW Myristate.
KW MYRISTATE.
FT CHAIN 1 201 NONSTRUCTURAL PROTEIN P20A.
FT CHAIN 202 286 COAT PROTEIN VP4.
FT CHAIN 287 504 COAT PROTEIN VP2.
FT CHAIN 505 724 COAT PROTEIN VP3.
FT CHAIN 725 938 COAT PROTEIN VP1.
FT CHAIN 939 954 COAT PROTEIN X.
FT CHAIN 955 1108 CORE PROTEIN P14.
FT CHAIN 1109 1426 CORE PROTEIN P41.
FT CHAIN 1427 1579 CORE PROTEIN P19.
FT CHAIN 1580 1602 GENOME-LINKED PROTEIN VPGL.
FT CHAIN 1603 1626 GENOME-LINKED PROTEIN VPGL.
FT CHAIN 1627 1650 GENOME-LINKED PROTEIN VPGL.
FT CHAIN 1651 1863 PROTEASE.
FT CHAIN 1864 2336 RNA-DIRECTED RNA POLYMERASE.
FT CHAIN 202 202 MYRISTATE (BY SIMILARITY).
SQ SEQUENCE 2336 AA; 259982 MM; 15AC2AB022B5B954 CRC64;

Query Match 48.5%; Score 48; DB 1; Length 2336;
Best Local Similarity 63.2%; Pred. No. 42;
Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 2 GSGVRGDSGLARVAROL 20
DB 865 GMGRGDLPELARVARAOL 883
RESULT 7
RS9_THEME STANDARD; PRT; 134 AA.
ID RS9_THEME
AC Q9X1G4;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S9.
GN RPS1 OR TM1453.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_Taxid=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.
RL Nature 399:323-329(1999).
CC -1- SIMILARITY: BELONGS TO THE S9P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL: AE001797; AAD36521.1; -
DR PIR: F72250; F72250.
DR TIGR: TM1453; -
DR HAMAP: MF_00532; -; 1.
DR InterPro: IPR007054; Ribosomal_S9.
DR Pfam: PF00380; Ribosomal_S9. 1.
DR ProDom: PD001627; Ribosomal_S9. 1.
DR PROSITE: PS00360; RIBOSOMAL_S9. 1.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 134 AA; 15198 MM; 698FB55B73E0A539 CRC64;
Query Match 46.5%; Score 46; DB 1; Length 134;
Best Local Similarity 47.4%; Pred. No. 47;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 2 GSGVRGDSGLARVAROL 20
DB 73 GSGLSGSGAVRGLARAL 91
RESULT 8
TRAD_HUMAN STANDARD; PRT; 312 AA.
AC Q15628;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor type 1 associated DEATH domain protein
DE (TNFR1-associated DEATH domain protein) (TNFRSF1A-associated via death

DE domain).
 GN TRADD.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95277836; PubMed=7758105;
 RA Hsu H., Xiong J., Goeddel D.V.;
 RT "The TNF receptor 1-associated protein TRADD signals cell death and
 NF-kappa B activation.";
 RL Cell 81:495-504(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Scheuepflug R., Dechant M., Fellenberg J., Everbeck V.,
 RA Debatin K.M.;
 RT "Sequence, genomic organisation, and mutation analysis of the human
 TRADD gene in childhood B- and T-lineage acute lymphoblastic leukemia
 and ALPS.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carroll P., Prange C.,
 RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP INTERACTION WITH RIPK1.
 RX MEDLINE=96200892; PubMed=8612133;
 RA Hsu H., Huang J., Shu H.-B., Baichwal V.R., Goeddel D.V.;
 RT "TNF-dependent recruitment of the protein kinase RIP to the TNF
 receptor-1 signaling complex.";
 RL Immunity 4:387-396(1996).
 RN [5]
 RP STRUCTURE BY NMR OF 1-179.
 RA Tseo D.H., McDonagh T., Telliez J.B., Hsu S., Malkian K., Xu G.Y.,
 RA Lin L.L.;
 RT "Solution structure of N-TRADD and characterization of the interaction
 between N-TRADD and C-TRAF2, a key step in the TNFR1 signaling pathway.";
 RL Mol. Cell 5:1051-1057(2000).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 1-179 IN COMPLEX WITH
 TRAF2.
 RX PubMed=10892748;
 RA Park Y.C., Ye H., Hala C., Segal D., Rich R.L., Liou H.C.,
 RA Myzaka D.G., Wu H.;
 RT "A novel mechanism of TRAF signaling revealed by structural and
 functional analyses of the TRADD-TRAF2 interaction.";
 RL Cell 101:777-787(2000).
 CC -1- FUNCTION: Adapter molecule for TNFRSF1A/TNFR1 that specifically
 associates with the cytoplasmic domain of activated TNFRSF1A/TNFR1
 mediating its interaction with FADD. Overexpression of TRADD leads
 to two major TNF-induced responses, apoptosis and activation of

CC NF-kappa-B.
 CC -1- SUBUNIT: Heterodimer with TNFRSF1A/TNFR1. Binds to TRAF2.
 CC Interacts with TRAF1, FADD and RIPK1.
 CC -1- TISSUE SPECIFICITY: Found in all examined tissues.
 CC -1- DOMAIN: Requires the intact DEATH domain to associate with
 CC TNFRSF1A/TNFR1.
 CC -1- SIMILARITY: Contains 1 death domain.
 CC -----
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 CC -----
 DR EMBL: LA1690; AAA98482.1; ALT-INIT.
 DR EMBL: AJ311614; CAC38018.2; -.
 DR EMBL: AJ311615; CAC38018.2; JOINED.
 DR EMBL: AJ311616; CAC38018.2; JOINED.
 DR EMBL: BC004491; AAH04491.1; -.
 DR PIR: A56911; A56911.
 DR PDB: 1F2H; 24-MAY-00.
 DR PDB: 1F3V; 06-JUN-00.
 DR Genew: HGNC:12030; TRADD.
 DR MIM: 603500; -.
 DR GO: GO:0006917; P:Induction of apoptosis; TAS.
 DR GO: GO:0007165; P:signal transduction; TAS.
 DR Interpro: IPR000488; Death.
 DR Pfam: PF00531; death; 1.
 DR SMART: SM00005; DEATH; 1.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR KMW Apoptosis; 3d-structure.
 FT DOMAIN 179 289 DEATH.
 FT POLY-PRO.
 FT SEQUENCE 312 AA; 34247 MW; 5645D7E63E5FF05A CRC64;
 QY 1 CGSGVGRGSGSLA 13
 DB 164 CGSGARGGGEVA 176
 ID POLG_FMDV1 STANDARD; PRT; 2333 AA.
 AC P03306; Q64768; Q84750; Q84751; Q84752; Q84753; Q84754; Q84760;
 AC Q84761; Q84762; Q84763; Q84764; Q84765; Q84766; Q84767; Q84768;
 AC Q84769; Q89824;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Genome polypeptide [contains: Nonstructural protein p20A; Coat
 DE Proteins VP1 TO VP4; Core protein p52; Genome-linked proteins VPg1 TO
 DE VPg3; Plicornain 3C (EC 3.4.22.28) (Protease 3C) (33C); RNA-directed
 DE RNA polymerase p56A (EC 2.7.7.48)];
 OS Foot-and-mouth disease virus (strain A10-61) (Aphthovirus A) (FMDV).
 CC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
 CC Aphthovirus.
 CC NCBI_TaxID=12112;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84169547; PubMed=6324120;
 RA Carroll A.R., Kowlands D.J., Clarke B.E.;
 RT "The complete nucleotide sequence of the RNA coding for the primary
 RT translation product of foot and mouth disease virus.";
 RL Nucleic Acids Res. 12:2461-2472(1984).
 RN [2]
 RP SEQUENCE OF 115-1048 FROM N.A.
 RX MEDLINE=82211814; PubMed=6282711;

[illegible]

| FT | VARIANT | 483 | 483 | S -> F (IN STRAIN CCRC 21164) |
|----|-----------------------|--------------------|---------------|-------------------------------|
| 50 | SEQUENCE | 512 AA: | 56527 MW: | 85/55252BC60F965 CRC64; |
| | Query Match | | 45.5%: | Score 45: DB 1: Length 512; |
| | Best Local Similarity | | 47.1%: | Pred. No. 25; |
| | Matches | 8: Conservative | 5: Mismatches | 4: Indels |
| Oy | 1 | CGSGVRGDSGSLALRYVA | 17 | |
| | | : :: :: | | |
| Db | 475 | CNSVIAGDSGSLSVSIS | 491 | |

| RESULT 12 | |
|---------------|------------|
| CH11_RHOSH | |
| ID CH11_RHOSH | STANDARD; |
| | PRT; 94 AA |

DT 01-MAY-1992 (Rel. 22, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 10 kDa chaperonin 1 (Protein Cpn10 1) (GROSS protein 1).
GN GROS1 OR GROS1 OR GROS.
OS Rhodospirillum rubrum.
OC Bacteria: Proteobacteria: Alphaproteobacteria: Rhodospirillales
OC Rhodospirillaceae: Rhodospirillum.
OX NCBI_TaxID=1063;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-HR;
RX MEDLINE=97144535; PubMed=8990302;
RA Lee W. T., Terlesky K.C., Tablita F.R.;
RT "Cloning and characterization of two groESL operons of *Rhodospirillum rubrum*.";
RT sphaeroids: transcriptional regulation of the heat-induced groESL operon";
RL J. Bacteriol. 179:487-495(1997).

RP SEQUENCE OF 1-22.
RX MEDLINE=91329399; PubMed=1678280,

RT "Purification and characterization of the chaperonin 10 and
RT chaperonin 60 proteins from *Rhodobacter sphaeroides*.";

CC -1- FUNCTION: Binds to Cpn60 in the presence of Mg-ATP and suppresses
CC the ATPase activity of the latter.

```

cc      similarity).
cc      -l- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
cc

```

CC -1 SIMILARITY: BELONGS TO THE GROES CHAPERONIN FAMILY.
CC -----
CC

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```
CC -----
DR EMBL; U37369; AABA1333.1; -.
DR HAMAP; MF_00580; -; 1.
DR InterPro; IPR001476; Chaprtn_Cpn10.
DR Pfam; PF00166; cpn10; 1.
DR PRINTS; PR00297; CHAPERONIN10.
DR ProDom; PD000566; Chaprtn_Cpn10; 1.
DR PROSITE; PS00681; CHAPERONINS_CPN10; 1.
DR KW Chaperone; Heat shock.
FT INIT_MET 94 AA; 10065 MW; 98B71231IDA8A86 CRC64;
SQ SEQUENCE 94 AA; 10065 MW; 98B71231IDA8A86 CRC64;
```

| | | | | |
|-----------------------|-------|----------------|-------|---------------|
| Query Match | 44.4% | Score 44; | DB 1; | Length 94; |
| Best Local Similarity | 66.7% | Pred. No. 6.5; | | |
| Matches | 8; | Conservative | 0; | Mismatches 4; |
| | | | | Indels 0; |
| | | | | Gaps 0; |

OY 1 CGSGVRGDSGSL 12
 DB 42 CGEGARKDSGSL 53

RESULT 13

CH10_RHOA STANDARD: PRT: 95 AA.
 AC Q93MH2;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 10 kDa chaperonin (Protein Cpn10) (gross protein).
 GN GP05 OR GP05.
 OS Rhodospirillum rubrum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Rhodospirillum rubrum.
 NCBI_TaxID=1076;

SEQUENCE FROM N.A.
 RA Xiao M., Zhu C.R., Qian X.M., Zheng P., Chen Y.Y.;
 RT Cloning and sequencing of the groESL operon of Rhodospirillum rubrum
 palustris.
 RT Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Binds to Cpn60 in the presence of Mg-ATP and suppresses
 the ATPase activity of the latter.
 CC -1- SUBUNIT: Heptamer of 7 subunits arranged in a ring (By
 similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE GP05 CHAPERONIN FAMILY.

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 or send an email to license@isb-sib.ch).

EMBL: AF406639; AAK94942.1; -
 DR HAMAP: MF_00580; -; 1.
 DR InterPro: IPR001476; Chaperin_Cpn10.
 DR Pfam: PF00166; cpn10; 1.
 DR PRINTS: PR00297; CHAPERONIN10.
 DR PRODOM: PD000566; Chaperin_Cpn10; 1.
 DR PROSITE: PS00681; CHAPERONIN_CPN10; 1.
 KW Chaperone.
 SQ SEQUENCE 95 AA; 10181 MW; EA3C1BA1E444015B CRC64;

Query Match 44.4%; Score 44; DB 1; Length 95;
 Best Local Similarity 66.7%; Pred. No. 6.6;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGSGVRGDSGSL 12
 DB 43 CGEGARKDSGSL 54

RESULT 14
 RS9_CYACA STANDARD: PRT: 128 AA.
 ID RS9_CYACA
 AC Q9TIV4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 GN Chloroplast 30S ribosomal protein S9.
 OS Rhodospirillum rubrum.
 OC Chloroplast.
 OC Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;
 OC Cyanidium.
 NCBI_TaxID=2771;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-RK-1;
 RX MEDLINE-20496959; PubMed-11040290;
 RA Gloeckner G., Rosenthal A., Valentini K.-U.;
 RT "The structure and gene repertoire of an ancient red algal plastid
 genome".
 RT J. Mol. Evol. 51:382-390(2000).
 CC -1- SIMILARITY: BELONGS TO THE S9P FAMILY OF RIBOSOMAL PROTEINS.

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EMBL: AF02186; AAF12930.1; -
 DR HAMAP: MF_00532; -; 1.
 DR InterPro: IPR000754; Ribosomal_S9.
 DR Pfam: PF00380; Ribosomal_S9; 1.
 DR PRODOM: PD001627; Ribosomal_S9; 1.
 DR PROSITE: PS00360; RIBOSOMAL_S9; FALSE_NEG.
 KW Ribosomal protein; Chloroplast.
 SQ SEQUENCE 128 AA; 14329 MW; DFFAA6345D38C8B CRC64;

Query Match 44.4%; Score 44; DB 1; Length 128;
 Best Local Similarity 42.1%; Pred. No. 8.9;
 Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 2 GSGVRGDSGSLARVAROL 20
 DB 67 GGGLSQAGAIRLARIARVL 85

RESULT 15
 RS9_MYCPCU STANDARD: PRT: 136 AA.
 ID RS9_MYCPCU
 AC Q98072;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 30S ribosomal protein S9.
 GN RPS1 OR MYPU_4960.
 OS Mycoplasma pulmonis.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 NCBI_TaxID=2107;
 RN [1]

SEQUENCE FROM N.A.
 RA STRAIN-UBB CTIP;
 RX MEDLINE-21267165; PubMed-11353084;
 RA Chamblaud I., Helling R., Ferris S., Barbe V., Samson D., Galisson F.,
 Mosser I., Dybviig K., Wroblewski H., Viari A., Rocha E.P.C.,
 Blanchard A.;
 RT "The complete genome sequence of the murine respiratory pathogen
 Mycoplasma pulmonis".
 RT Nucleic Acids Res. 29:2145-2153(2001).
 CC -1- SIMILARITY: BELONGS TO THE S9P FAMILY OF RIBOSOMAL PROTEINS.

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EMBL: AL445564; CAC13669.1; -
 DR PIR: H90573; H90573.
 DR Mypulist: MYPU_4960; -
 DR HAMAP: MF_00532; -; 1.
 DR InterPro: IPR000754; Ribosomal_S9.
 DR Pfam: PF00380; Ribosomal_S9; 1.

Thu Oct 9 10:26:16 2003

us-09-549-186b-9.rsp

Page 9

DR ProDom: PD001627; Ribosomal_S9; 1.
DR PROSITE; PS00360; RIBOSOMAL_S9; 1.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 136 AA; 15268 MW; 78EB9CC47D51DF1 CRC64;

| | | | | |
|-----------------------|--------|----------------|-------|---------------|
| Query Match | 44.48; | Score 44; | DB 1; | Length 136; |
| Best Local Similarity | 42.18; | Pred. No. 9.4; | | |
| Matches | 8; | Conservative | 5; | Mismatches 6; |
| | | | | Indels 0; |
| | | | | Gaps 0; |

```
QY      2 GSGVRGDSGLALRVARQL 20
        | | : | : | : | : | |
Db      75 GGGLAGQAGAIRLGIARAL 93
```

Search completed: October 9, 2003, 10:15:00
Job time : 12.3333 secs

Search completed: October 9, 2003, 10:15:00
job time : 12.3333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 10:09:40 ; Search time 49.3333 Seconds
(without alignments)
104.616 Million cell updates/sec

Title: US-09-549-186b-9
Perfect score: 99
Sequence: 1 GSGVGRDGSGLARVAROL 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriophage:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------|-------------|
| 1 | 83.8 | 20 | 12 | 09PX4 | foot-and-mo |
| 2 | 70.7 | 213 | 12 | 0912L2 | foot-and-mo |
| 3 | 70.7 | 213 | 12 | 067446 | foot-and-mo |
| 4 | 70.7 | 213 | 12 | 067448 | foot-and-mo |
| 5 | 70.7 | 213 | 12 | 065093 | foot-and-mo |
| 6 | 67.7 | 213 | 12 | 098V26 | foot-and-mo |
| 7 | 66.7 | 210 | 12 | 067438 | foot-and-mo |
| 8 | 66.7 | 969 | 12 | 0902N6 | foot-and-mo |
| 9 | 64.6 | 126 | 12 | 08V443 | foot-and-mo |
| 10 | 64.6 | 169 | 12 | 067442 | foot-and-mo |
| 11 | 60.6 | 125 | 12 | 08V442 | foot-and-mo |
| 12 | 60.6 | 143 | 12 | 09XP00 | foot-and-mo |
| 13 | 60.6 | 208 | 12 | 08JUR8 | foot-and-mo |
| 14 | 60.6 | 211 | 12 | 08JUP0 | foot-and-mo |
| 15 | 60.6 | 212 | 12 | 08JUP1 | foot-and-mo |
| 16 | 60.6 | 213 | 12 | 08JUS6 | foot-and-mo |

| | | | | | |
|----|------|-----|----|--------|-------------|
| 17 | 60.6 | 213 | 12 | 08JUM1 | foot-and-mo |
| 18 | 60.6 | 213 | 12 | 08JUP9 | foot-and-mo |
| 19 | 60.6 | 213 | 12 | 08JUP7 | foot-and-mo |
| 20 | 60.6 | 213 | 12 | 08JUP4 | foot-and-mo |
| 21 | 60.6 | 213 | 12 | 0912L1 | foot-and-mo |
| 22 | 60.6 | 213 | 12 | 08JUP5 | foot-and-mo |
| 23 | 60.6 | 213 | 12 | 08JUL1 | foot-and-mo |
| 24 | 60.6 | 213 | 12 | 08JUL0 | foot-and-mo |
| 25 | 60.6 | 213 | 12 | 08JUP5 | foot-and-mo |
| 26 | 60.6 | 213 | 12 | 08JUP0 | foot-and-mo |
| 27 | 60.6 | 213 | 12 | 08JUP3 | foot-and-mo |
| 28 | 60.6 | 213 | 12 | 08JUP2 | foot-and-mo |
| 29 | 60.6 | 213 | 12 | 08JUP1 | foot-and-mo |
| 30 | 60.6 | 213 | 12 | 08JUL0 | foot-and-mo |
| 31 | 60.6 | 213 | 12 | 08JUP7 | foot-and-mo |
| 32 | 60.6 | 213 | 12 | 08JUP0 | foot-and-mo |
| 33 | 60.6 | 213 | 12 | 08JUP3 | foot-and-mo |
| 34 | 60.6 | 213 | 12 | 08JUP8 | foot-and-mo |
| 35 | 60.6 | 213 | 12 | 08JUP9 | foot-and-mo |
| 36 | 60.6 | 213 | 12 | 08JUP0 | foot-and-mo |
| 37 | 60.6 | 213 | 12 | 08JUP5 | foot-and-mo |
| 38 | 58.6 | 197 | 12 | 08JUP2 | foot-and-mo |
| 39 | 58.6 | 213 | 12 | 08JUP4 | foot-and-mo |
| 40 | 58.6 | 652 | 12 | 09Q2N8 | foot-and-mo |
| 41 | 57.6 | 213 | 12 | 08JUP9 | foot-and-mo |
| 42 | 57.6 | 213 | 12 | 0912K6 | foot-and-mo |
| 43 | 57.6 | 213 | 12 | 066924 | foot-and-mo |
| 44 | 57.6 | 213 | 12 | 0912K4 | foot-and-mo |
| 45 | 57.6 | 213 | 12 | 0912L0 | foot-and-mo |

ALIGNMENTS

| | |
|--|---|
| RESULT 1 | |
| 09PX4 | PRELIMINARY; PRT; 20 AA. |
| AC 09PX4; | |
| DT 01-MAY-2000 (TREMBLrel. 13, Created) | |
| DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update) | |
| DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update) | |
| DE VP1 protein (Fragment). | |
| OS Foot-and-mouth disease virus. | |
| OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; | |
| OC Aphthovirus. | |
| CC NCBI_TaxID=12110; | |
| RN [1] | |
| RP SEQUENCE FROM N.A. | |
| RX MEDLINE=96100820; PubMed=7483796; | |
| RA Piattoli P., Hassard S., Newman J.F., Brown F.; | |
| RT "Antigenic variants in a plaque-isolate of foot-and-mouth disease virus: implications for vaccine production."; | |
| RL Vaccine 13:781-784(1995). | |
| SO SEQUENCE 20 AA; 1925 MW; E91F87C99C19D7DB CRC64; | |
| Query Match | 83.8%; Score 83; DB 12; Length 20; |
| Best Local Similarity | 94.7%; Pred. No. 3.2e-06; |
| Matches | 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0; |
| OY | 2 GSGVGRDGSGLARVAROL 20 |
| DB | 1 GSGVGRDGSGLARVAROL 19 |
| RESULT 2 | |
| 0912L2 | PRELIMINARY; PRT; 213 AA. |
| ID 0912L2; | |
| AC 0912L2; | |
| DT 01-DEC-2001 (TREMBLrel. 19, Created) | |
| DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update) | |
| DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update) | |
| DE VP1 protein (Fragment). | |
| GN ID. | |

OS Foot-and-mouth disease virus A.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12110;
RN [1]
RP SOURCE FROM N.A.
RC STRAIN-A Arg/68;
RX MEDLINE=2130796; PubMed=11724271;
RA Konig G.A., Blanco C., Knowles N.J., Palma E.L., Maradel E.,
RA Piccone M.E.;
RT "Phylogenetic analysis of foot-and-mouth disease viruses isolated in
RT Argentina";
RL Virus Genes 23:175-182(2001).
DR EMBL: AJ308694; CAC48168.1; -;
DR InterPro: IPR004080; FMDVPIcoat.
DR InterPro: IPR001676; Rhv.
DR Pfam: PF00073; rhv; 1.
DR PRINTS: PR01542; FMDVPIcoat.
FT NON_TER 1 1
FT SEQUENCE 213 AA; 23488 MW; 203FECB8A45EECE CRC64;

Query Match 70.7%; Score 70; DB 12; Length 213;
Best Local Similarity 78.9%; Pred. No. 0.0048;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 GSGVRDGSGLARVAROL 20
Db 140 GSGRGDMGSLARVAROL 158

RESULT 3
O67446 PRELIMINARY; PRT; 213 AA.
ID 067446
AC 067446; 067447;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Foot and mouth disease virus (Serotype Aven76), capsid protein VP1
DE mRNA (Fragment).
OS Foot-and-mouth disease virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12110;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85190547; PubMed=2986125;
RA Meddell G.N., Yansura D.G., Dowbenko D.J., Hoatlin M.E., Grubman M.J.,
RA Moore D.M., Kleid D.G.;
RT "Sequence variation in the gene for the immunogenic capsid protein VP1
RT of foot-and-mouth disease virus type A";
RL Proc. Natl. Acad. Sci. U.S.A. 82:2618-2622(1985).
DR EMBL: K03344; AAA42600.1; -;
DR InterPro: IPR004080; FMDVPIcoat.
DR InterPro: IPR001676; Rhv.
DR Pfam: PF00073; rhv; 1.
DR PRINTS: PR01542; FMDVPIcoat.
FT NON_TER 1 1
FT SEQUENCE 213 AA; 23311 MW; C4ED4E0116A0DB8A CRC64;

Query Match 70.7%; Score 70; DB 12; Length 213;
Best Local Similarity 78.9%; Pred. No. 0.0048;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 GSGVRDGSGLARVAROL 20
Db 140 GSGRGDMGSLARVAROL 158

RESULT 4
O67448 PRELIMINARY; PRT; 213 AA.
ID 067448

AC 067448; 067449;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Foot and mouth disease virus (Serotype Aarg79), capsid protein VP1
DE mRNA (Fragment).
OS foot-and-mouth disease virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12110;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85190547; PubMed=2986125;
RA Meddell G.N., Yansura D.G., Dowbenko D.J., Hoatlin M.E., Grubman M.J.,
RA Moore D.M., Kleid D.G.;
RT "Sequence variation in the gene for the immunogenic capsid protein VP1
RT of foot-and-mouth disease virus type A";
RL Proc. Natl. Acad. Sci. U.S.A. 82:2618-2622(1985).
DR EMBL: K03345; AAA42601.1; -;
DR InterPro: IPR004080; FMDVPIcoat.
DR InterPro: IPR001676; Rhv.
DR Pfam: PF00073; rhv; 1.
DR PRINTS: PR01542; FMDVPIcoat.
FT NON_TER 1 1
FT SEQUENCE 213 AA; 23345 MW; 546C7FF78CD45CC0 CRC64;

Query Match 70.7%; Score 70; DB 12; Length 213;
Best Local Similarity 78.9%; Pred. No. 0.0048;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 GSGVRDGSGLARVAROL 20
Db 140 GSGRGDMGSLARVAROL 158

RESULT 5
O65093 PRELIMINARY; PRT; 213 AA.
ID 065093
AC 065093;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Foot and mouth disease virus strain A Venceslau VP1 (Fragment).
DE Foot-and-mouth disease virus.
OS Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12110;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85077620; PubMed=6096217;
RA Cheung A., Whitehead P., Weiss S., Kupper H.;
RT "Nucleotide sequence of the VP1 gene of the foot-and-mouth disease
RT virus strain A Venceslau";
RL Gene 30:241-245(1984).
DR EMBL: M12905; AAA42663.1; -;
DR InterPro: IPR004080; FMDVPIcoat.
DR InterPro: IPR001676; Rhv.
DR Pfam: PF00073; rhv; 1.
DR PRINTS: PR01542; FMDVPIcoat.
FT NON_TER 1 1
FT SEQUENCE 213 AA; 23327 MW; 04808BD9571D7073 CRC64;

Query Match 70.7%; Score 70; DB 12; Length 213;
Best Local Similarity 78.9%; Pred. No. 0.0048;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 GSGVRDGSGLARVAROL 20
Db 140 GSGRGDMGSLARVAROL 158

RP SEQUENCE FROM N.A.
RC STRAIN-KEN/1/76;
RA van Rensburg H.G., Bastos A.D., Haydon D., Joubert F., Nel L.H.;
RT "Gene heterogeneity in the leader and 3C proteinases of foot-and-mouth disease virus."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF390861; AAL73359.1; -
DR InterPro: IPR004080; FMDVPIcoat.
DR InterPro: IPR001676; Rhv.
DR Pfam: PF00073; rhv; 1.
DR PRINTS: PR01542; FMDVPIcoat.
FT NON_TER 1 1
FT SEQUENCE 126 126
SQ SEQUENCE 126 AA; 13693 MW; 82675FAC45E713BB CRC64;
Query Match
Best Local Similarity 77.8%; Score 64; DB 12; Length 126;
Pred. No. 0.024;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 GSGVGDGSLAARVAKOL 20
Db 54 GSGRGDGLAARVAKOL 71
RESULT 10
O67442 PRELIMINARY; PRT; 169 AA.
AC 067442; 067443;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Foot and mouth disease virus (Serotype A32), capsid protein VP1 mRNA
OS Foot-and-mouth disease virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12110;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85190547; PubMed=2986125;
RA Meddell G.N., Yansura D.G., Dowbenko D.J., Hoatlin M.E., Grubman M.J.,
RA Moore D.M., Kleid D.G.;
RT "Sequence variation in the gene for the immunogenic capsid protein VP1
of foot-and-mouth disease virus type A."
RL Proc. Natl. Acad. Sci. U.S.A. 82:2618-2622(1985).
DR EMBL: K03342; AAA42598.1; -
DR HSSP: Q88571; 1TME.
DR InterPro: IPR004080; FMDVPIcoat.
DR InterPro: IPR001676; Rhv.
DR Pfam: PF00073; rhv; 2.
DR PRINTS: PR01542; FMDVPIcoat.
FT NON_TER 1 1
FT SEQUENCE 169 169
SQ SEQUENCE 169 AA; 18499 MW; 9E8AEDC94AC57F67 CRC64;
Query Match
Best Local Similarity 73.7%; Score 64; DB 12; Length 169;
Pred. No. 0.033;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12111;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GAM/51/98;
RA van Rensburg H.G., Bastos A.D., Haydon D., Joubert F., Nel L.H.;
RT "Gene heterogeneity in the leader and 3C proteinases of foot-and-mouth disease virus."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF390862; AAL73360.1; -
DR InterPro: IPR004080; FMDVPIcoat.
DR InterPro: IPR001676; Rhv.
DR Pfam: PF00073; rhv; 1.
DR PRINTS: PR01542; FMDVPIcoat.
FT NON_TER 1 1
FT SEQUENCE 125 125
SQ SEQUENCE 125 AA; 13486 MW; 2D172B9F0C281A02 CRC64;
Query Match
Best Local Similarity 73.7%; Score 60; DB 12; Length 125;
Pred. No. 0.1;
Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 GSGVGDGSLAARVAKOL 20
Db 53 GSTRGDGSLAARVAKOL 71
RESULT 12
O9YP00 PRELIMINARY; PRT; 143 AA.
AC 09YP00;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE VP1 protein (Fragment).
CN VP1.
OS Foot-and-mouth disease virus A.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12111;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NM/X2/64;
RA Liu Z., Zhao Q., Liu W., Xie Q.;
RT "Analysis of VP1 coding nucleotide sequences of six strains of foot-and-mouth disease virus type A."
RL Ping Tu Hsueh Pao 14:60-67(1998).
DR EMBL: AJ131664; CAA10474.1; -
DR InterPro: IPR004080; FMDVPIcoat.
DR InterPro: IPR001676; Rhv.
DR Pfam: PF00073; rhv; 1.
DR PRINTS: PR01542; FMDVPIcoat.
FT NON_TER 1 1
FT SEQUENCE 143 143
SQ SEQUENCE 143 AA; 15881 MW; CF0CC1858CC331E0 CRC64;
Query Match
Best Local Similarity 72.2%; Score 60; DB 12; Length 143;
Pred. No. 0.12;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

RESULT 11
O8V442 PRELIMINARY; PRT; 125 AA.
AC 08V442;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE VP1 (Fragment).
OS Foot-and-mouth disease virus A.

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DE 1D protein (Fragment).
GN POL.
OS Foot-and-mouth disease virus A.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12111;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A/IND/170/88;
RX MEDLINE-21954626; PubMed-11958451;
RA Tosh C., Sanval A., Hemadri D., Venkataramanan R.;
RT "Phylogenetic analysis of serotype A foot-and-mouth disease virus
isolated in India between 1977 and 2000.";
RL Arch. Virol. 147:493-513(2002).
DR EMBL; AF390612; AAM63984.1;
DR InterPro; IPR004080; FMDVPicoat.
DR Pfam; PF00073; rhv; 1.
DR PRINTS; PRO1542; FMDVPicoat.
FT NON_TER 1
SQ SEQUENCE 208 AA; 22607 MW; 6CE616F86E60CF7E CRC64;

Query Match 60.6%; Score 60; DB 12; Length 208;
Best Local Similarity 68.4%; Pred. No. 0.18;
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 GSGVGDGSGSLARVROL 20
DB 140 GAGRRGDLGALAAVAAQL 158

RESULT 14
O8JUP0 PRELIMINARY; PRT; 211 AA.
AC O8JUP0;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE 1D protein (Fragment).
GN POL.
OS Foot-and-mouth disease virus A.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12111;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A/IND/302/88;
RX MEDLINE-21954626; PubMed-11958451;
RA Tosh C., Sanval A., Hemadri D., Venkataramanan R.;
RT "Phylogenetic analysis of serotype A foot-and-mouth disease virus
isolated in India between 1977 and 2000.";
RL Arch. Virol. 147:493-513(2002).
DR EMBL; AF390641; AAM64012.1;
DR InterPro; IPR004080; FMDVPicoat.
DR Pfam; PF00073; rhv; 1.
DR PRINTS; PRO1542; FMDVPicoat.
FT NON_TER 1
SQ SEQUENCE 211 AA; 23100 MW; CBFEC94CCDD9E2EE3 CRC64;

Query Match 60.6%; Score 60; DB 12; Length 211;
Best Local Similarity 68.4%; Pred. No. 0.18;
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 GSGVGDGSGSLARVROL 20
DB 140 GTGRRGDLGALAAVAAQL 158

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RESULT 15
O8JUP1

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ID O8JUP1 PRELIMINARY; PRT; 212 AA.
AC O8JUP1;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE 1D protein (Fragment).
GN POL.
OS Foot-and-mouth disease virus A.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Aphthovirus.
OX NCBI_TaxID=12111;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A/IND/299/99;
RX MEDLINE-21954626; PubMed-11958451;
RA Tosh C., Sanval A., Hemadri D., Venkataramanan R.;
RT "Phylogenetic analysis of serotype A foot-and-mouth disease virus
isolated in India between 1977 and 2000.";
RL Arch. Virol. 147:493-513(2002).
DR EMBL; AF390640; AAM64011.1;
DR InterPro; IPR004080; FMDVPicoat.
DR Pfam; PF00073; rhv; 1.
DR PRINTS; PRO1542; FMDVPicoat.
FT NON_TER 1
SQ SEQUENCE 212 AA; 23150 MW; E6B690890042CD3A CRC64;

Query Match 60.6%; Score 60; DB 12; Length 212;
Best Local Similarity 68.4%; Pred. No. 0.18;
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 GSGVGDGSGSLARVROL 20
DB 139 GTGRRGDLGALAAVAAQL 157

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Search completed: October 9, 2003, 10:17.35
Job time : 50.3333 secs

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OM protein - protein search, using sw model

Run on: October 9, 2003, 10:11:24 ; Search time 17.3333 Seconds
(without alignments)
48.820 Million cell updates/sec

Title: US-09-549-186B-9
Perfect score: 99
Sequence: 1 CGSGVRGDSGLALVARQL 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
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5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 99 | 100.0 | 20 | 4 | US-08-716-249-9 |
| 2 | 93 | 93.9 | 20 | 4 | US-08-716-249-8 |
| 3 | 86 | 86.9 | 20 | 4 | US-08-716-249-7 |
| 4 | 86 | 86.9 | 31 | 1 | US-08-418-716A-3 |
| 5 | 84.5 | 85.4 | 19 | 4 | US-08-716-249-1 |
| 6 | 77 | 77.8 | 35 | 3 | US-09-100-600A-1 |
| 7 | 77 | 77.8 | 46 | 3 | US-09-100-600A-38 |
| 8 | 77 | 77.8 | 75 | 3 | US-09-100-600A-28 |
| 9 | 74 | 74.7 | 31 | 1 | US-08-418-716A-4 |
| 10 | 73 | 73.7 | 31 | 1 | US-08-418-716A-5 |
| 11 | 73 | 73.7 | 31 | 1 | US-08-418-716A-6 |
| 12 | 71.5 | 72.2 | 19 | 4 | US-08-716-249-2 |
| 13 | 71 | 71.7 | 31 | 1 | US-08-418-716A-2 |
| 14 | 70 | 70.7 | 31 | 1 | US-08-418-716A-1 |
| 15 | 70 | 70.7 | 31 | 1 | US-08-418-716A-7 |
| 16 | 70 | 70.7 | 46 | 3 | US-09-100-600A-42 |
| 17 | 70 | 70.7 | 46 | 3 | US-09-100-600A-49 |
| 18 | 70 | 70.7 | 46 | 3 | US-09-100-600A-50 |
| 19 | 69 | 69.7 | 35 | 3 | US-09-100-600A-2 |
| 20 | 69 | 69.7 | 35 | 3 | US-09-100-600A-8 |
| 21 | 69 | 69.7 | 46 | 3 | US-09-100-600A-3 |
| 22 | 69 | 69.7 | 65 | 3 | US-09-100-600A-27 |
| 23 | 69 | 69.7 | 75 | 3 | US-09-100-600A-29 |
| 24 | 66 | 66.7 | 46 | 3 | US-09-100-600A-43 |
| 25 | 66 | 66.7 | 46 | 3 | US-09-100-600A-44 |
| 26 | 66 | 66.7 | 46 | 3 | US-09-100-600A-45 |
| 27 | 64 | 64.6 | 46 | 3 | US-09-100-600A-48 |

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|----|----|------|-----|---|----------------------|--------------------|
| 28 | 61 | 61.6 | 35 | 3 | US-09-100-600A-9 | Sequence 9, Appl1 |
| 29 | 61 | 61.6 | 55 | 3 | US-09-100-600A-33 | Sequence 33, Appl1 |
| 30 | 58 | 58.6 | 46 | 3 | US-09-100-600A-39 | Sequence 39, Appl1 |
| 31 | 57 | 57.6 | 46 | 3 | US-09-100-600A-46 | Sequence 46, Appl1 |
| 32 | 53 | 53.5 | 45 | 3 | US-09-100-600A-55 | Sequence 55, Appl1 |
| 33 | 53 | 53.5 | 45 | 3 | US-09-100-600A-65 | Sequence 65, Appl1 |
| 34 | 52 | 52.5 | 45 | 3 | US-09-100-600A-60 | Sequence 60, Appl1 |
| 35 | 52 | 52.5 | 46 | 3 | US-09-100-600A-67 | Sequence 67, Appl1 |
| 36 | 50 | 50.5 | 170 | 4 | US-09-732-210-1676 | Sequence 1676, Ap |
| 37 | 50 | 50.5 | 387 | 4 | US-09-252-991A-17881 | Sequence 17881, A |
| 38 | 49 | 49.5 | 45 | 3 | US-09-100-600A-51 | Sequence 51, Appl1 |
| 39 | 49 | 49.5 | 45 | 3 | US-09-100-600A-52 | Sequence 52, Appl1 |
| 40 | 49 | 49.5 | 45 | 3 | US-09-100-600A-62 | Sequence 62, Appl1 |
| 41 | 49 | 49.5 | 45 | 3 | US-09-100-600A-64 | Sequence 64, Appl1 |
| 42 | 48 | 48.5 | 46 | 3 | US-09-100-600A-40 | Sequence 40, Appl1 |
| 43 | 48 | 48.5 | 45 | 3 | US-09-100-600A-41 | Sequence 41, Appl1 |
| 44 | 46 | 46.5 | 46 | 3 | US-09-100-600A-56 | Sequence 56, Appl1 |
| 45 | 46 | 46.5 | 312 | 1 | US-08-41A-625-2 | Sequence 2, Appl1 |

ALIGNMENTS

RESULT 1
US-08-716-249-9
; Sequence 9, Application US/08716249
; Patent No. 6455244
; GENERAL INFORMATION:
; APPLICANT: Guichard, Gilles
; APPLICANT: Muller, Sylviane
; APPLICANT: Briand, Jean-Paul
; APPLICANT: Regemortel, Marc
; TITLE OF INVENTION: Retropeptides, Antibodies Thereof, and
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Spencer & Frank
; STREET: 1100 New York Avenue, Suite 300E
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,249
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR95/00292
; FILING DATE: 13-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Calvet, Frederick F.
; REGISTRATION NUMBER: 28,557
; REFERENCE/DOCKET NUMBER: GROFO 7001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)414-4000
; TELEFAX: (202)414-4040
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; US-08-716-249-9
Query Match 100.0%; Score 99; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGSGVRDGSGLARVARQL 20
Db 1 CGSGVRDGSGLARVARQL 20

RESULT 2

US-08-716-249-8
Sequence 8, Application US/08716249
Patent No. 6455244
GENERAL INFORMATION:
APPLICANT: Guichard, Gilles
APPLICANT: Muller, Sylviane
APPLICANT: Briand, Jean-Paul
APPLICANT: Regemortel, Marc
TITLE OF INVENTION: Retropeptides, Antibodies Thereof, and
TITLE OF INVENTION: Uses Thereof for Vaccination and In Vitro Diagnostics
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spencer & Frank
STREET: 1100 New York Avenue, Suite 300E
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,249
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/00292
FILING DATE: 13-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Calvetti, Frederick F.
REGISTRATION NUMBER: 28,557
REFERENCE/DOCKET NUMBER: GROFO 7001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)414-4000
TELEFAX: (202)414-4040
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
ANTI-SENSE: YES
US-08-716-249-8
Query Match 93.9%; Score 93; DB 4; Length 20;
Best Local Similarity 95.0%; Pred. No. 8,7e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CGSGVRDGSGLARVARQL 20
Db 1 CGSGVRDGSGLARVARQL 20
RESULT 3
US-08-716-249-7
Sequence 7, Application US/08716249
Patent No. 6455244
GENERAL INFORMATION:
APPLICANT: Guichard, Gilles
APPLICANT: Muller, Sylviane
APPLICANT: Briand, Jean-Paul
APPLICANT: Regemortel, Marc
TITLE OF INVENTION: Retropeptides, Antibodies Thereof, and
TITLE OF INVENTION: Uses Thereof for Vaccination and In Vitro Diagnostics

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spencer & Frank
STREET: 1100 New York Avenue, Suite 300E
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,249
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/00292
FILING DATE: 13-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Calvetti, Frederick F.
REGISTRATION NUMBER: 28,557
REFERENCE/DOCKET NUMBER: GROFO 7001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)414-4000
TELEFAX: (202)414-4040
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-716-249-7

Query Match 86.9%; Score 86; DB 4; Length 20;
Best Local Similarity 90.0%; Pred. No. 9,8e-07;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 CGSGVRDGSGLARVARQL 20
Db 1 CGSGVRDGSGLARVARQL 20

RESULT 4

US-08-418-716A-3
Sequence 3, Application US/08418716A
Patent No. 5612040
GENERAL INFORMATION:
APPLICANT: Mason, Peter W.
APPLICANT: Baxt, Barry
APPLICANT: Reider, Elizabeth
APPLICANT: Bernstein, Analia
APPLICANT: Kang, Angray S
TITLE OF INVENTION: No. 5612040-Infectious Foot-and-Mouth Disease
TITLE OF INVENTION: Viruses
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janelle S. Graeter
STREET: Rm. 411, Bldg. 005, BARC-W
CITY: Beltsville
STATE: Maryland
COUNTRY: USA
ZIP: 20705
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,716A
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Graeter, Janelle S.
REGISTRATION NUMBER: 35,024
REFERENCE/DOCKET NUMBER: 0137.94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 504-5060
TELEFAX: (301) 504-6629
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Foot and mouth disease virus
US-08-418-716A-3

Query Match 86.9%; Score 86; DB 1; Length 31;
Best Local Similarity 94.7%; Pred. No. 1.6e-06;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGVRGDSGSLALVARQL 20
|||||
DB 11 GSGVRGDSGSLALVARQL 29

RESULT 5
US-08-716-249-1
Sequence 1, Application US/08716249
Patent No. 6455244
GENERAL INFORMATION:
APPLICANT: Gulchard, Gilles
APPLICANT: Muller, Sylviane
APPLICANT: Briand, Jean-Paul
APPLICANT: Regemortel, Marc
TITLE OF INVENTION: Retropeptides, Antibodies Thereof, and
TITLE OF INVENTION: Uses Thereof for Vaccination and In Vitro Diagnosis
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spencer & Frank
STREET: 1100 New York Avenue, Suite 300E
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,249
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/00292
FILING DATE: 13-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Calveti, Frederick F.
REGISTRATION NUMBER: 28,557
REFERENCE/DOCKET NUMBER: GROFO 7001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)414-4000
TELEFAX: (202)414-4040
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-716-249-1

Query Match 85.4%; Score 84.5; DB 4; Length 19;
Best Local Similarity 95.0%; Pred. No. 1.6e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CGSGVRGDSGSLALVARQL 20
|||||
DB 1 CGSGVRGDSGSLALVARQL 19

RESULT 6
US-09-100-600A-1
Sequence 1, Application US/09100600A
Patent No. 6107021
GENERAL INFORMATION:
APPLICANT: Wang, Chang YI
APPLICANT: Shen, Ming
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR
TITLE OF INVENTION: FOOT-AND-MOUTH DISEASE
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Flanagan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,600A
FILING DATE: 20-Jun-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4156
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-600A-1

Query Match 77.8%; Score 77; DB 3; Length 35;
Best Local Similarity 89.5%; Pred. No. 4e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSGVRGDSGSLALVARQL 20
|||||
DB 7 GSGVRGDSGSLALVARQL 25

RESULT 7
US-09-100-600A-38
Sequence 38, Application US/09100600A
Patent No. 6107021
GENERAL INFORMATION:
APPLICANT: Wang, Chang YI
APPLICANT: Shen, Ming
TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR
TITLE OF INVENTION: FOOT-AND-MOUTH DISEASE
NUMBER OF SEQUENCES: 91

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Morgan & Flanagan, L.L.P.
;; STREET: 345 Park Avenue
;; CITY: New York
;; STATE: NY
;; COUNTRY: USA
;; ZIP: 10154-0054
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: Windows 95
;; SOFTWARE: Word 97
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/100,600A
;; FILING DATE: 20-Jun-1998
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Maria C.H. Lin
;; REGISTRATION NUMBER: 29,323
;; REFERENCE/DOCKET NUMBER: 1151-4156
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-758-4800
;; TELEFAX: 212-751-6849
;; INFORMATION FOR SEQ ID NO: 38:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 46 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-09-100-600A-38

Query Match 77.8%; Score 77; DB 3; Length 46;
Best Local Similarity 89.5%; Pred. No. 5.3e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSGVRDGSGLAPVAROL 20
Db 16 GSGVRDGSGLAPVAROL 34

RESULT 8
US-09-100-600A-28
; Sequence 28, Application US/09100600A
; Patent No. 6107021
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; APPLICANT: Shen, Ming
; TITLE OF INVENTION: SYNTHETIC PEPTIDE VACCINES FOR
; TITLE OF INVENTION: FOOT-AND-MOUTH DISEASE
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Flanagan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,600A
; FILING DATE: 20-Jun-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4156
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849

;; INFORMATION FOR SEQ ID NO: 28:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 75 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-09-100-600A-28

Query Match 77.8%; Score 77; DB 3; Length 75;
Best Local Similarity 89.5%; Pred. No. 8.9e-05;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSGVRDGSGLAPVAROL 20
Db 47 GSGVRDGSGLAPVAROL 65

RESULT 9
US-08-418-716A-4
; Sequence 4, Application US/08418716A
; Patent No. 5612040
; GENERAL INFORMATION:
; APPLICANT: Mason, Peter W.
; APPLICANT: Baxt, Barry
; APPLICANT: Reider, Elizabeth
; APPLICANT: Berinstein, Analia
; APPLICANT: Kang, Angray S
; TITLE OF INVENTION: No. 5612040-Infectious Foot-and-Mouth Disease
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janelle S. Graeter
; STREET: Rm. 411, Bldg. 005, BARC-W
; CITY: Beltsville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20705
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentia Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/418,716A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Graeter, Janelle S.
; REGISTRATION NUMBER: 35,024
; REFERENCE/DOCKET NUMBER: 0137.94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 504-6629
; TELEFAX: (301) 504-5060
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: Internal
; ORGANISM: Foot and mouth disease virus
;; US-08-418-716A-4

Query Match 74.7%; Score 74; DB 1; Length 31;
Best Local Similarity 84.2%; Pred. No. 0.0001;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSGVRDGSGLAPVAROL 20
Db 11 GSGVRDGSGLAPVAROL 29

RESULT 10
US-08-418-716A-5
Sequence 5, Application US/08418716A
Patent No. 5612040
GENERAL INFORMATION:
APPLICANT: Mason, Peter W.
APPLICANT: Baxt, Barry
APPLICANT: Reider, Elizabeth
APPLICANT: Bernstein, Analia
APPLICANT: Kang, Angray S
TITLE OF INVENTION: No. 5612040- Infectious Foot-and-Mouth Disease
TITLE OF INVENTION: Viruses
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janelle S. Graeter
STREET: Rm. 411, Bldg. 005, BARC-W
CITY: Beltsville
STATE: Maryland
COUNTRY: USA
ZIP: 20705
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,716A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Graeter, Janelle S.
REGISTRATION NUMBER: 35,024
REFERENCE/DOCKET NUMBER: 0137.94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 504-6629
TELEFAX: (301) 504-5060
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Foot and mouth disease virus
US-08-418-716A-5
Query Match 73.7%; Score 73; DB 1; Length 31;
Best Local Similarity 84.2%; Pred. No. 0.00014;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 GSGVGRGDSGLAPVARQL 20
DB 11 GSGVGRGDSGLAPVARQL 29
RESULT 11
US-08-418-716A-6
Sequence 6, Application US/08418716A
Patent No. 5612040
GENERAL INFORMATION:
APPLICANT: Mason, Peter W.
APPLICANT: Baxt, Barry
APPLICANT: Reider, Elizabeth
APPLICANT: Bernstein, Analia
APPLICANT: Kang, Angray S
TITLE OF INVENTION: No. 5612040- Infectious Foot-and-Mouth Disease
TITLE OF INVENTION: Viruses
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESSEE: Janelle S. Graeter
STREET: Rm. 411, Bldg. 005, BARC-W
CITY: Beltsville
STATE: Maryland
COUNTRY: USA
ZIP: 20705
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,716A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Graeter, Janelle S.
REGISTRATION NUMBER: 35,024
REFERENCE/DOCKET NUMBER: 0137.94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 504-6629
TELEFAX: (301) 504-5060
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Foot and mouth disease virus
US-08-418-716A-6
Query Match 73.7%; Score 73; DB 1; Length 31;
Best Local Similarity 84.2%; Pred. No. 0.00014;
Matches 16; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 GSGVGRGDSGLAPVARQL 20
DB 11 GSGVGRGDSGLAPVARQL 29
RESULT 12
US-08-716-249-2
Sequence 2, Application US/08716249
Patent No. 6455244
GENERAL INFORMATION:
APPLICANT: Gulchard, Gillies
APPLICANT: Muller, Sylviane
APPLICANT: Briand, Jean-Paul
APPLICANT: Regenmortel, Marc
TITLE OF INVENTION: Retropeptides, Antibodies Thereof, and
TITLE OF INVENTION: Uses Thereof for Vaccination and In Vitro Diagnosis
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spencer & Frank
STREET: 1100 New York Avenue, Suite 300E
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,249
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: NO PCT/FR95/00292
FILING DATE: 13-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Calvetti, Frederick F.
REGISTRATION NUMBER: 28,557
REFERENCE/DOCKET NUMBER: GROFO 7001
TELEPHONE: (202)414-4000
TELEFAX: (202)414-4040
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-716-249-2

Query Match 72.2%; Score 71.5; DB 4; Length 19;
Best Local Similarity 85.0%; Pred. No. 0.00014;
Matches 17; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 GSGVRGDSGLARVAROL 20
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DB 1 GSGVRGDSGLARVAROL 19

RESULT 13
US-08-418-716A-2
Sequence 2, Application US/08418716A
Patent No. 5612040
GENERAL INFORMATION:
APPLICANT: Mason, Peter W.
APPLICANT: Baxt, Barry
APPLICANT: Reider, Elizabeth
APPLICANT: Bernstein, Analia
APPLICANT: Kang, Angray S
TITLE OF INVENTION: No. 5612040-Infectious Foot-and-Mouth Disease
TITLE OF INVENTION: Viruses
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janelle S. Graeter
STREET: Rm. 411, Bldg. 005, BARC-W
CITY: Beltsville
STATE: Maryland
COUNTRY: USA
ZIP: 20705
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,716A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Graeter, Janelle S.
REGISTRATION NUMBER: 35,024
REFERENCE/DOCKET NUMBER: 0137.94
TELEPHONE: (301) 504-6629
TELEFAX: (301) 504-5060
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Foot and mouth disease virus
US-08-418-716A-1

ORIGINAL SOURCE:
ORGANISM: Foot and mouth disease virus
US-08-418-716A-2

Query Match 71.7%; Score 71; DB 1; Length 31;
Best Local Similarity 84.2%; Pred. No. 0.00028;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GSGVRGDSGLARVAROL 20
||||||| |||||
DB 11 GSGVRGDSGLARVAROL 29

RESULT 14
US-08-418-716A-1
Sequence 1, Application US/08418716A
Patent No. 5612040
GENERAL INFORMATION:
APPLICANT: Mason, Peter W.
APPLICANT: Baxt, Barry
APPLICANT: Reider, Elizabeth
APPLICANT: Bernstein, Analia
APPLICANT: Kang, Angray S
TITLE OF INVENTION: No. 5612040-Infectious Foot-and-Mouth Disease
TITLE OF INVENTION: Viruses
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janelle S. Graeter
STREET: Rm. 411, Bldg. 005, BARC-W
CITY: Beltsville
STATE: Maryland
COUNTRY: USA
ZIP: 20705
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,716A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Graeter, Janelle S.
REGISTRATION NUMBER: 35,024
REFERENCE/DOCKET NUMBER: 0137.94
TELEPHONE: (301) 504-6629
TELEFAX: (301) 504-5060
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Foot and mouth disease virus
US-08-418-716A-1

Query Match 70.7%; Score 70; DB 1; Length 31;
Best Local Similarity 84.2%; Pred. No. 0.0004;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GSGVRGDSGLARVAROL 20
||||||| |||||
DB 11 GSGVRGDSGLARVAROL 29

RESULT 15
US-08-418-716A-7

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; Sequence 7, Application US/08418716A
; Patent No. 5612040
; GENERAL INFORMATION:
; APPLICANT: Mason, Peter W.
; APPLICANT: Baxt, Barry
; APPLICANT: Reider, Elizabeth
; APPLICANT: Berinstein, Analia
; APPLICANT: Kang, Angray S
; TITLE OF INVENTION: No. 5612040-Infectious Foot-and-Mouth Disease
; TITLE OF INVENTION: Viruses
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janelle S. Graeter
; STREET: Rm. 411, Bldg. 005, BARC-W
; CITY: Beltsville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20705
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/418,716A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Graeter, Janelle S.
; REGISTRATION NUMBER: 35,024
; REFERENCE/DOCKET NUMBER: 0137.94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 504-6629
; TELEFAX: (301) 504-5060
; INFORMATION FOR SEQ. ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE:
; ORGANISM: Foot and mouth disease virus
; US-08-418-716A-7

Query Match 70.7%; Score 70; DB 1; Length 31;
Best Local Similarity 78.9%; Pred. No. 0.0004;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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OY 2 GSGVGRDGSIALVAROL 20
||||:|:|||||
Db 11 GSGVKGEGSIALPRVAROL 29

Search completed: October 9, 2003, 10:19:38
Job time : 17.333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 9, 2003, 10:14:31 ; Search time 21.333 Seconds

(without alignments)
151.058 Million cell updates/sec

Title: US-09-549-186b-9

Perfect score: 99

Sequence: 1 GSGVGRGDSGSLRVARQL 20

Scoring table: BLAST62

Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCP_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/PCPUS_PUBCOMB.pep:*

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8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|---------------------|---------------------|
| 1 | 50.5 | 173 | 15 | US-10-156-761-12492 | Sequence 12492, A |
| 2 | 46.5 | 312 | 15 | US-10-207-655-186 | Sequence 186, App |
| 3 | 46.5 | 359 | 9 | US-09-988-200-2 | Sequence 2, App11 |
| 4 | 45.5 | 1208 | 15 | US-10-156-761-13251 | Sequence 13251, A |
| 5 | 44.4 | 74 | 15 | US-10-106-698-7642 | Sequence 7642, A |
| 6 | 43.4 | 294 | 15 | US-10-102-806-595 | Sequence 595, App |
| 7 | 42.4 | 508 | 11 | US-09-895-298-92 | Sequence 92, App1 |
| 8 | 42.4 | 1014 | 9 | US-08-912-020-266 | Sequence 266, App |
| 9 | 41.4 | 87 | 10 | US-09-764-877-1521 | Sequence 1521, App |
| 10 | 41.4 | 261 | 15 | US-10-156-761-9294 | Sequence 9294, App1 |
| 11 | 41.4 | 449 | 10 | US-09-919-497-89 | Sequence 89, App1 |
| 12 | 41.4 | 458 | 9 | US-09-925-301-1282 | Sequence 1282, App |
| 13 | 41.4 | 459 | 10 | US-09-925-300-1440 | Sequence 1440, App |
| 14 | 41.4 | 532 | 11 | US-09-941-947A-38 | Sequence 38, App1 |
| 15 | 41.4 | 532 | 15 | US-10-209-372-2 | Sequence 2, App11 |

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|----|------|------|------|----|---------------------|--------------------|
| 16 | 41 | 41.4 | 722 | 14 | US-10-128-870-23 | Sequence 23, App1 |
| 17 | 41 | 41.4 | 722 | 15 | US-10-131-685-23 | Sequence 23, App1 |
| 18 | 41 | 41.4 | 3500 | 15 | US-10-153-219-2 | Sequence 2, App1 |
| 19 | 41 | 41.4 | 3537 | 15 | US-10-153-219-15 | Sequence 15, App1 |
| 20 | 40.5 | 40.9 | 378 | 12 | US-10-166-225A-49 | Sequence 49, App1 |
| 21 | 40 | 40.4 | 182 | 10 | US-09-738-626-4147 | Sequence 4147, App |
| 22 | 40 | 40.4 | 216 | 9 | US-09-908-180-4 | Sequence 4, App11 |
| 23 | 40 | 40.4 | 274 | 10 | US-09-738-626-6076 | Sequence 6076, App |
| 24 | 40 | 40.4 | 283 | 15 | US-10-156-761-9949 | Sequence 9949, App |
| 25 | 40 | 40.4 | 316 | 15 | US-10-106-698-5711 | Sequence 5711, App |
| 26 | 40 | 40.4 | 337 | 9 | US-09-815-242-11926 | Sequence 11926, A |
| 27 | 40 | 40.4 | 350 | 11 | US-09-847-208-53 | Sequence 53, App1 |
| 28 | 40 | 40.4 | 390 | 9 | US-09-925-297-531 | Sequence 531, App |
| 29 | 40 | 40.4 | 476 | 9 | US-09-291-299A-3 | Sequence 3, App11 |
| 30 | 40 | 40.4 | 627 | 15 | US-10-222-100-3 | Sequence 3, App11 |
| 31 | 40 | 40.4 | 784 | 9 | US-09-905-983-52 | Sequence 52, App1 |
| 32 | 40 | 40.4 | 784 | 12 | US-10-021-660-99 | Sequence 99, App1 |
| 33 | 40 | 40.4 | 865 | 11 | US-09-842-758-20 | Sequence 20, App1 |
| 34 | 40 | 40.4 | 934 | 11 | US-09-842-758-18 | Sequence 18, App1 |
| 35 | 40 | 40.4 | 1783 | 12 | US-10-276-934-12 | Sequence 12, App1 |
| 36 | 40 | 40.4 | 1800 | 12 | US-10-276-934-10 | Sequence 10, App1 |
| 37 | 40 | 40.4 | 1826 | 12 | US-10-276-934-9 | Sequence 9, App1 |
| 38 | 40 | 40.4 | 2008 | 12 | US-10-276-934-11 | Sequence 11, App1 |
| 39 | 40 | 40.4 | 2306 | 12 | US-10-276-934-14 | Sequence 14, App1 |
| 40 | 40 | 40.4 | 2352 | 12 | US-10-276-934-13 | Sequence 12, App1 |
| 41 | 39.5 | 39.9 | 446 | 10 | US-09-738-626-6262 | Sequence 6262, App |
| 42 | 39.5 | 39.9 | 531 | 15 | US-10-156-761-13662 | Sequence 13662, A |
| 43 | 39 | 39.4 | 89 | 9 | US-09-925-301-1058 | Sequence 1058, App |
| 44 | 39 | 39.4 | 89 | 15 | US-10-106-698-5417 | Sequence 5417, App |
| 45 | 39 | 39.4 | 124 | 16 | US-10-080-170-376 | Sequence 376, App |

ALIGNMENTS

RESULT 1

US-10-156-761-12492

Sequence 12492, Application US/10156761

Publication No. US20030119018A1

GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI

APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAWA, JUN

APPLICANT: HORIKAWA, HIROSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SAKAKI, YOSHIYUKI

APPLICANT: HATTORI, MASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR FILING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 12492

LENGTH: 173

TYPE: PRN

ORGANISM: Streptomyces avermitilis

US-10-156-761-12492

Query Match 50.5%; Score 50; DB 15; Length 173;

Best local similarity 57.9%; Pred. No. 5.3;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 GSGVGRGDSGSLRVARQL 20

DB 111 GSGVGRGDSGSLRVARQL 129

RESULT 2

US-10-207-655-186

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? Sequence 186, Application US/10207655
? Publication No. US20030118592A1
? GENERAL INFORMATION:
? APPLICANT: Ledbetter, Jeffrey A.
? APPLICANT: Hayden-Ledbetter, Martha S.
? TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
? FILE REFERENCE: 390069.401C1
? CURRENT APPLICATION NUMBER: US/10/207,655
? CURRENT FILING DATE: 2002-07-25
? NUMBER OF SEQ ID NOS: 426
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 186
? LENGTH: 312
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-10-207-655--186

OY      1 CGSGVGRGDSGLA 13
        ||||| 11 1 :1
Query Match      46.5%; Score 46; DB 15; Length 312;
Best Local Similarity 61.5%; Pred. No. 40;
Matches      8; Conservative      1; Mismatches      4; Indels      0; Gaps      0;

Db      164 CGSGARGGDGEVA 176

RESULT 3
US-09-988-200-2
? Sequence 2, Application US/09988200
? Patent No. US2002009453A1
? GENERAL INFORMATION:
? APPLICANT: BARBEYRON, Tristan
? POTIN, Philippe
? RICHARD, Christophe
? HENRISSAT, Bernard
? YVIN, Jean-Claude
? KLOAREG, Bernard
? TITLE OF INVENTION: glycolyse hydrolase genes and their
? use for producing enzymes for the biodegradation of
? carraegeenans
? NUMBER OF SEQUENCES: 8
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: DENNISON, MESEROLE, SCHEINER & SCHULTZ
? STREET: 612 Crystal Square 4, 1745 Jefferson Davis
? Highway
? CITY: ARLINGTON
? STATE: VIRGINIA
? COUNTRY: U.S.A.
? ZIP: 22202
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/988,200
? FILING DATE: 19-NO. US2002009453A1-2001
? CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 09/269,731
? FILING DATE: <Unknown>
? APPLICATION NUMBER: FR 96 12204
? FILING DATE: 07-OCT-1996
? ATTORNEY/AGENT INFORMATION:
? NAME: IRA SCHULTZ
? REGISTRATION NUMBER: <Unknown>
? REFERENCE/DOCKET NUMBER: <Unknown>
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703) 412-1155
? TELEFAX: (703) 412-1161
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 559 amino acids

```

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: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-988-200-2

Query Match          46.5%; Score 46; DB 9; Length 559;
Best Local Similarity 64.3%; Pred. No. 75;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 CGSGVRCDSGLAL 14
   ||| || ||| : |
Db 298 CGSAVRSDSGFVEL 311

RESULT 4
US-10-156-761-13251
: Sequence 13251, Application US/10156761
: Publication No. US20030119018A1
: GENERAL INFORMATION:
: APPLICANT: OMURA, SATOSHI
: APPLICANT: IKEDA, HARUO
: APPLICANT: ISHIKAWA, JUN
: APPLICANT: HORIKAWA, HIROSHI
: APPLICANT: SHIBA, TADAYOSHI
: APPLICANT: SAKAKI, YOSHIYUKI
: APPLICANT: HATTORI, MASAHIRA
: TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
: FILE REFERENCE: 249-262
: CURRENT APPLICATION NUMBER: US/10/156,761
: PRIOR FILING DATE: 2002-05-29
: PRIOR APPLICATION NUMBER: JP 2001-204089
: PRIOR FILING DATE: 2001-05-30
: PRIOR APPLICATION NUMBER: JP 2001-272697
: PRIOR FILING DATE: 2001-08-02
: NUMBER OF SEQ ID NOS: 15109
: SEQ ID NO 13251
: LENGTH: 1208
: TYPE: PRT
: ORGANISM: Streptomyces avermitilis
US-10-156-761-13251

Query Match          45.5%; Score 45; DB 15; Length 1208;
Best Local Similarity 81.8%; Pred. No. 2; 5e+02;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 7 GDSGSLALRYA 17
   |||||:||||:|
Db 623 GDSGTLALRYA 633

RESULT 5
US-10-106-698-7642
: Sequence 7642, Application US/10106698
: Publication No. US20030109690A1
: GENERAL INFORMATION:
: APPLICANT: Ruben et al.
: TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
: FILE REFERENCE: PA00591
: CURRENT APPLICATION NUMBER: US/10/106,698
: PRIOR FILING DATE: 2002-03-27
: PRIOR APPLICATION NUMBER: PCT/US00/26524
: PRIOR FILING DATE: 2000-09-28
: PRIOR APPLICATION NUMBER: US 60/157,137
: PRIOR FILING DATE: 1999-09-29
: PRIOR APPLICATION NUMBER: US 60/163,280
: PRIOR FILING DATE: 1999-11-03
: NUMBER OF SEQ ID NOS: 8564
: SOFTWARE: PatentIn Ver. 3.0
: SEQ ID NO 7642
: LENGTH: 74
: TYPE: PRT
: ORGANISM: Homo sapiens

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FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (49)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (54)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-7642

Query Match      44.4%; Score 44; DB 15; Length 74;
Best Local Similarity 57.9%; Pred. No. 17;
Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY      1 CGSG-VRGDGSGLALRYA 17
      ||| : | ||| | |
DB      26 CGSSRDHLGSGSLALRYA 44

RESULT 6
US-10-102-806-595
; Sequence 595, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 595
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (269)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (278)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-595

Query Match      43.4%; Score 43; DB 15; Length 294;
Best Local Similarity 53.3%; Pred. No. 11e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      3 SGVRGDSGLALRYA 17
      || || | | | | |
DB      159 SGTSGDHGELVYVRIA 173

RESULT 7
US-09-895-298-92
; Sequence 92, Application US/09895298
; Publication No. US20030078405A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 47 Human Secreted Proteins
; FILE REFERENCE: P2035P1
; CURRENT APPLICATION NUMBER: US/09/895,298
; CURRENT FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: 09/591,16
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: PCT/US89/29950
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/113,006
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; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/112,809
; PRIOR FILING DATE: 1998-12-17,
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-298-92

Query Match      42.4%; Score 42; DB 11; Length 508;
Best Local Similarity 56.2%; Pred. No. 2.8e+02;
Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1 CGSGVRGDSGLALRY 16
      |||| | | | | |
DB      215 CGSGENDRGEOALPY 230

RESULT 8
US-09-912-020-266
; Sequence 266, Application US/09912020
; Patent No. US20020045592A1
; GENERAL INFORMATION:
; APPLICANT: Zyskind, Judith
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Trawick, John
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Frielelch, Jamie M.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
; FILE REFERENCE: ELITRA.001DVI
; CURRENT APPLICATION NUMBER: US/09/912,020
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: 09/492,709
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/117,405
; PRIOR FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 485
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 266
; LENGTH: 1014
; TYPE: PRT
; ORGANISM: E. COLI
US-09-912-020-266

Query Match      42.4%; Score 42; DB 9; Length 1014;
Best Local Similarity 40.0%; Pred. No. 5.8e+02;
Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY      1 CGSGVRGDSGLALRYA 20
      || | | | | | | |
DB      165 CASGASNETGMLTQFARSL 184

RESULT 9
US-09-764-877-1521
; Sequence 1521, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PAM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1521
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LENGTH: 87
TYPE: PRT
ORGANISM: Homo sapiens
US-09-764-877-1521

Query Match 41.4%; Score 41; DB 10; Length 87;
Best Local Similarity 88.9%; Pred. No. 58;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSGVRGDSG 10
||| |||||
DB 22 GSGVRGDSG 30

RESULT 10
US-10-156-761-9294
Sequence 9294, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASHIIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9294
LENGTH: 261
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-9294

Query Match 41.4%; Score 41; DB 15; Length 261;
Best Local Similarity 52.6%; Pred. No. 1.9e+02;
Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 GSGVRGDSGSLARVAROL 20
||| |||||
DB 97 GSGVLDIGTAVYRLAROL 115

RESULT 11
US-09-919-497-89
Sequence 89, Application US/09919497
Patent No. US20020106662A1
GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn version 3.0
SEQ ID NO 89
LENGTH: 449
TYPE: PRT
ORGANISM: Homo sapiens
US-09-919-497-89

Query Match 41.4%; Score 41; DB 10; Length 449;
Best Local Similarity 53.8%; Pred. No. 3.4e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGSGVRGDSGSLA 13
||| |||||
DB 37 CGGDVKGSGGYVA 49

RESULT 12
US-09-925-301-1282
Sequence 1282, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1282
LENGTH: 458
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (249)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1282

Query Match 41.4%; Score 41; DB 9; Length 458;
Best Local Similarity 53.8%; Pred. No. 3.5e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGSGVRGDSGSLA 13
||| |||||
DB 46 CGGDVKGSGGYVA 58

RESULT 13
US-09-925-300-1440
Sequence 1440, Application US/09925300
Patent No. US20020151681A1
GENERAL INFORMATION:
APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1440
LENGTH: 459
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-300-1440

Query Match 41.4%; Score 41; DB 10; Length 459;
Best Local Similarity 62.5%; Pred. No. 3.5e+02;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 VRGDSGSLARVAROL 20
||| |||||
DB 61 VRGSGASARRSARSL 76

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RESULT 14
US-09-941-947A-38
; Sequence 38, Application US/09941947A
; Publication NO. US20030003528A1
; GENERAL INFORMATION:
; APPLICANT: Brzostowicz, Patricia C.
; APPLICANT: Cheng, Qilong
; APPLICANT: Dicosimo, Deana J.
; APPLICANT: Koffas, Matheos
; APPLICANT: Miller, Edward S. Jr.
; APPLICANT: Odom, J. Martin
; APPLICANT: Picataggio, Steve
; APPLICANT: Rouverie, Pierre E.
; TITLE OF INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE
; FILE REFERENCE: CL1903 US NA
; CURRENT APPLICATION NUMBER: US/09/941,947A
; CURRENT FILING DATE: 2001-09-01
; PRIOR APPLICATION NUMBER: 60/229,907
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,858
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 38
; LENGTH: 532
; TYPE: PR
; ORGANISM: Rhodococcus erythropolis AN12
US-09-941-947A-38

Query Match 41.4%; Score 41; DB 11; Length 532;
Best Local Similarity 56.2%; Pred. No. 4.1e+02;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 GSGVRGDSGLALRYA 17
| | | | | | | | | |
Db 498 GGGVSGASGRSAARIA 513

RESULT 15
US-10-209-372-2
; Sequence 2, Application US/10209372
; Publication NO. US20030100045A1
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours, Inc.
; APPLICANT: Cheng, Qilong
; APPLICANT: Tao, Luan
; TITLE OF INVENTION: CAROTENOID KETOGLASE GENE
; FILE REFERENCE: CL-1849 US NA
; CURRENT APPLICATION NUMBER: US/10/209,372
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 532
; TYPE: PR
; ORGANISM: Rhodococcus erythropolis AN12
US-10-209-372-2

Query Match 41.4%; Score 41; DB 15; Length 532;
Best Local Similarity 56.2%; Pred. No. 4.1e+02;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 GSGVRGDSGLALRYA 17
| | | | | | | | | |
Db 498 GGGVSGASGRSAARIA 513
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Search completed: October 9, 2003, 10:20:49
Job time : 22.333 secs

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